

Result	Query				
No.	score	Match	length	DB	ID

Description					

1	489	100.0	489	6	AR0043268
2	489	100.0	489	6	AR0243439
3	489	100.0	489	6	AR070281
4	489	100.0	489	6	AR085740
5	489	100.0	489	6	AR122046
6	489	100.0	489	6	AR122868
7	489	100.0	489	6	AR125105
8	489	100.0	489	6	AX006786
9	489	100.0	489	6	AX320244
10	489	100.0	489	6	AX320244
11	489	100.0	489	6	125783
12	489	100.0	489	6	128849
13	489	100.0	489	6	162692
14	489	100.0	489	6	179219
15	489	100.0	489	6	AR103280
16	489	100.0	489	6	AX024715
17	489	100.0	489	6	AX301227
18	489	100.0	489	6	AX301227
19	487.4	99.7	489	6	HS014407
20	487.4	99.7	489	6	AR094449
21	481	98.4	489	6	BD008811
22	481	98.4	489	6	BD008812
23	466.6	95.4	489	6	AR094650
24	466.6	95.4	489	6	AX320242
25	465	95.1	489	6	AR024348
26	465	95.1	489	6	BD000555
27	465	95.1	489	6	AR004267
28	465	95.1	489	6	AR024348
29	465	95.1	489	6	AR070282
30	465	95.1	489	6	AR085741
31	465	95.1	489	6	AR122045
32	465	95.1	489	6	AR122867
33	465	95.1	489	6	AR125104
34	465	95.1	489	6	AX006785
35	465	95.1	489	6	AX006785
36	465	95.1	489	6	125782
37	451.4	92.3	489	6	128850
38	394.6	80.7	489	6	179220
39	386.6	79.1	489	6	CAU03099
40	386.6	79.1	489	6	HS115MR
41	380	77.7	489	6	BTU04243
42	380	77.7	489	6	AF108148
43	378.6	77.4	489	6	ASU05142
44	378.4	77.4	489	6	HS115MR1
45	378.4	77.4	489	6	X94222
					H.sapiens m
					AF149700
					Ovis arie
					AR087004
					Sequence
					AF031167
					Homo sapi

	RESULT	1		DNA	linear	PAT 04-DEC-1998
	LOCUS	AR004268		489 bp		
	DEFINITION	Sequence 4 from patent US 5747024.				
	ACCSSION	AR004268				
	VERSION	AR004268.1 GI:3965147				
	KEYWORDS	.				
	SOURCE	. Unknown.				
	ORGANISM	. Unclassified.				
	REFERENCE	1 (bases 1 to 489)				
	AUTHORS	Grabstein,K.H. and Widmer,M.B.				
	TITLE	Vaccine adjuvant comprising interleukin-15				
	JOURNAL	patent: US 5747024-A 4 05-MAY-1998;				
	FEATURES	Location/Qualifiers				
	source	1..489				
BASE COUNT	/organism="unknown"	159 a 79 c 95 g 156 t				
ORIGIN						

Query Match	100.0%;	Score 489;	DB 6;	Length 489
Best Local Similarity	100.0%;	Pred. No. 1.2e-92;		

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACCAATTTGAGAAATTTCCATCCAGTGTACTGTGTTACTT 60
 Db 1 ATGAGATTTCGAACCAATTTGAGAAATTTCCATCCAGTGTACTGTGTTACTT 60
 QY 61 CTAACAGTCAATTTCTAACTGAGAGTGCATTCATGTCTTCAATTTGGGCTGTTCACT 120
 Db 61 CTAACAGTCAATTTCTAACTGAGAGTGCATTCATGTCTTCAATTTGGGCTGTTCACT 120
 QY 121 GCAGGCTTCCTAAACAGAACCACTGGGTGAATGTAAATGATTTGAAAAAATT 180
 Db 121 GCAGGCTTCCTAAACAGAACCACTGGGTGAATGTAAATGATTTGAAAAAATT 180
 QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATAGGAAAGATGATGTTAC 240
 Db 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATAGGAAAGATGATGTTAC 240
 QY 241 CCCAGTTGCAAGTACAGCAATGAAAGTCTTCTCTGGAGTTCAAGTTATTTCACTT 300
 Db 241 CCCAGTTGCAAGTACAGCAATGAAAGTCTTCTCTGGAGTTCAAGTTATTTCACTT 300
 QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGAAATGATGATCCTAGCAAAACAC 360
 Db 301 GAGTCGGAGATGCAAGTATTCATGATACAGAAATGATGATCCTAGCAAAACAC 360
 QY 361 AGTTGCTCTTAAATGGAATGTACAGAAATCTGATGCAAAAGATGAGAACTGGAG 420
 Db 361 AGTTGCTCTTAAATGGAATGTACAGAAATCTGATGCAAAAGATGAGAACTGGAG 420
 QY 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGCCAAATGTTCAATCAC 480
 Db 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGCCAAATGTTCAATCAC 480
 QY 481 ACTTCTTGA 489
 Db 481 ACTTCTTGA 489

RESULT 2
 LOCUS AR024349 489 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 2 from patent US 5795966.
 ACCESSION AR024349
 VERSION AR024349.1 GI:3977643
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 489)
 AUTHORS Grabstein, K.H., Pettit, D.K. and Paxton, R.J.
 TITLE Antagonists of Interleukin-15
 JOURNAL Patent: US 5795966-A 2 18-AUG-1998;
 FEATURES
 source Location/Qualifiers
 1..489
 BASE COUNT 159 a 79 c 95 g 156 t
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACCAATTTGAGAAATTTCCATCCAGTGTACTGTGTTACTT 60
 Db 1 ATGAGATTTCGAACCAATTTGAGAAATTTCCATCCAGTGTACTGTGTTACTT 60
 QY 61 CTAACAGTCAATTTCTAACTGAGAGTGCATTCATGTCTTCAATTTGGGCTGTTCACT 120
 Db 61 CTAACAGTCAATTTCTAACTGAGAGTGCATTCATGTCTTCAATTTGGGCTGTTCACT 120
 QY 121 GCAGGCTTCCTAAACAGAACCACTGGGTGAATGTAAATGATTTGAAAAAATT 180
 Db 121 GCAGGCTTCCTAAACAGAACCACTGGGTGAATGTAAATGATTTGAAAAAATT 180

Db 121 GCAGGCTTCCTAAACAGAACCACTGGGTGAATGTAAATGATTTGAAAAAATT 180
 QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATAGGAAAGATGATGTTAC 240
 Db 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATAGGAAAGATGATGTTAC 240
 QY 241 CCCAGTTGCAAGTACAGCAATGAAAGTCTTCTCTGGAGTTCAAGTTATTTCACTT 300
 Db 241 CCCAGTTGCAAGTACAGCAATGAAAGTCTTCTCTGGAGTTCAAGTTATTTCACTT 300
 QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGAAATGATGATCCTAGCAAAACAC 360
 Db 301 GAGTCGGAGATGCAAGTATTCATGATACAGAAATGATGATCCTAGCAAAACAC 360
 QY 361 AGTTGCTCTTAAATGGAATGTACAGAAATCTGATGCAAAAGATGAGAACTGGAG 420
 Db 361 AGTTGCTCTTAAATGGAATGTACAGAAATCTGATGCAAAAGATGAGAACTGGAG 420
 QY 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGCCAAATGTTCAATCAC 480
 Db 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGCCAAATGTTCAATCAC 480
 QY 481 ACTTCTTGA 489
 Db 481 ACTTCTTGA 489

RESULT 3
 LOCUS AR070281 489 bp DNA linear PAT 18-FEB-2000
 DEFINITION Sequence 1 from patent US 5892001.
 ACCESSION AR070281
 VERSION AR070281.1 GI:7221169
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 489)
 AUTHORS Grabstein, K.H., Anderson, D.M., Eisenman, J.R., Fung, V. and Rauch, C.
 TITLE Epithelium-derived T-cell factor antibodies
 JOURNAL Patent: US 5892001-A 1 06-APR-1999;
 FEATURES
 source Location/Qualifiers
 1..489
 BASE COUNT 159 a 79 c 95 g 156 t
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACCAATTTGAGAAATTTCCATCCAGTGTACTGTGTTACTT 60
 Db 1 ATGAGATTTCGAACCAATTTGAGAAATTTCCATCCAGTGTACTGTGTTACTT 60
 QY 61 CTAACAGTCAATTTCTAACTGAGAGTGCATTCATGTCTTCAATTTGGGCTGTTCACT 120
 Db 61 CTAACAGTCAATTTCTAACTGAGAGTGCATTCATGTCTTCAATTTGGGCTGTTCACT 120
 QY 121 GCAGGCTTCCTAAACAGAACCACTGGGTGAATGTAAATGATTTGAAAAAATT 180
 Db 121 GCAGGCTTCCTAAACAGAACCACTGGGTGAATGTAAATGATTTGAAAAAATT 180
 QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATAGGAAAGATGATGTTAC 240
 Db 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATAGGAAAGATGATGTTAC 240
 QY 241 CCCAGTTGCAAGTACAGCAATGAAAGTCTTCTCTGGAGTTCAAGTTATTTCACTT 300
 Db 241 CCCAGTTGCAAGTACAGCAATGAAAGTCTTCTCTGGAGTTCAAGTTATTTCACTT 300

QY 301 GAGTCGGAGATGCAAGTATTGATGATAGAGAAATCTGATCATCTAGCAAAAC 360
 DB 301 GAGTCGGAGATGCAAGTATTGATGATAGAGAAATCTGATCATCTAGCAAAAC 360
 QY 361 AGTTGCTCTTAATGGAATGTAACAGATCTGATGCAAGAAATGAGAACTGGAG 420
 DB 361 AGTTGCTCTTAATGGAATGTAACAGATCTGATGCAAGAAATGAGAACTGGAG 420
 QY 421 GAAAAAATTTTAAGAAATTTTGGAGGTTTGTACATATGTCCTCAATGTCATCAAC 480
 DB 421 GAAAAAATTTTAAGAAATTTTGGAGGTTTGTACATATGTCCTCAATGTCATCAAC 480
 QY 481 ACTTCTTGA 489
 DB 481 ACTTCTTGA 489
 RESULT 4
 LOCUS AR085740 489 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 1 from patent US 5985262.
 ACCESSION AR085740
 VERSION AR085740.1 GI:10012506
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 489)
 AUTHORS Grabstein, K.H., Anderson, D.M., Eisenman, J.R., Fung, V. and Rauch, C.
 TITLE Method of treatment with epithelium derived T-cell factor
 JOURNAL Patent: US 5985262-A 1 16-NOV-1999;
 FEATURES
 source location/Qualifiers
 1. 489
 /organism="unknown"
 BASE COUNT 159 a 79 c 95 g 156 t
 ORIGIN
 Query Match 100.0%; Score 489; DB 6; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 ACTTCTTGA 489
 DB 481 ACTTCTTGA 489
 RESULT 5
 LOCUS AR122046 489 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 2 from patent US 6165466.
 ACCESSION AR122046
 VERSION AR122046.1 GI:14106363
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 489)
 AUTHORS Grabstein, K.H., Pettit, D.K. and Paxton, R.J.
 TITLE Antagonists of interleukin-15
 JOURNAL Patent: US 6165466-A 2 26-DEC-2000;
 FEATURES
 source location/Qualifiers
 1. 489
 /organism="unknown"
 BASE COUNT 159 a 79 c 95 g 156 t
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAGAAATTTGAAACCAATTTGAGAGATTTTCATCCAGTCTCTGTTTACTT 60
 DB 1 ATGAGAAATTTGAAACCAATTTGAGAGATTTTCATCCAGTCTCTGTTTACTT 60
 QY 61 CTAACAGTCAATTTCTAAGTGAAGCTGCAATTCATGCTTCTTGGCTGTTTCACT 120
 DB 61 CTAACAGTCAATTTCTAAGTGAAGCTGCAATTCATGCTTCTTGGCTGTTTCACT 120
 QY 121 GCAGGCTTCTTAAGCAAGAACCACTGGGTGAATGTAATGATTTGAAAAAATT 180
 DB 121 GCAGGCTTCTTAAGCAAGAACCACTGGGTGAATGTAATGATTTGAAAAAATT 180
 QY 181 GAAGATCTTATTCATCTATGATATGATGCTACTTATATACGAAAGTATGTTTCA 240
 DB 181 GAAGATCTTATTCATCTATGATATGATGCTACTTATATACGAAAGTATGTTTCA 240
 QY 241 CCAGTTGCAAGTAAACCAATGCAATGAGTCTTCTTGGAGTTTCAAGTTATTTCACTT 300
 DB 241 CCAGTTGCAAGTAAACCAATGCAATGAGTCTTCTTGGAGTTTCAAGTTATTTCACTT 300
 QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAGAAATCTGATCATCTAGCAAAAC 360
 DB 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAGAAATCTGATCATCTAGCAAAAC 360
 QY 361 AGTTGCTCTTAATGGAATGTAACAGATCTGATGCAAGAAATGAGAACTGGAG 420
 DB 361 AGTTGCTCTTAATGGAATGTAACAGATCTGATGCAAGAAATGAGAACTGGAG 420
 QY 421 GAAAAAATTTTAAGAAATTTTGGAGGTTTGTACATATGTCCTCAATGTCATCAAC 480
 DB 421 GAAAAAATTTTAAGAAATTTTGGAGGTTTGTACATATGTCCTCAATGTCATCAAC 480
 QY 481 ACTTCTTGA 489
 DB 481 ACTTCTTGA 489
 RESULT 6
 LOCUS AR122868 489 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 2 from patent US 6168783.
 ACCESSION AR122868

VERSION ARI22868.1 GI:14107834
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 489)
 AUTHORS Grabsstein,K.H., Pettit,D.K. and Paxton,R.J.
 TITLE Antagonists of Interleukin-15
 JOURNAL Patent: US 6168783-A 2 02-JAN-2001;
 FEATURES
 source location/Qualifiers
 1..489
 /organism="unknown"
 BASE COUNT 159 a 79 c 95 g 156 t
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACCCATTTGAGAGATTTCCATCCAGTCTACTTGTTCATT 60
 DB 1 ATGAGATTTCGAACCCATTTGAGAGATTTCCATCCAGTCTACTTGTTCATT 60
 QY 61 CTAACAGCTATTTTCTAATCTAAGCTGCATTCATCTTCAATTTGGCTGTTCACT 120
 DB 61 CTAACAGCTATTTTCTAATCTAAGCTGCATTCATCTTCAATTTGGCTGTTCACT 120
 QY 121 GCAGGCTTCCTTAAACAGAACCCAGTGGTGATGTAATAGATTTGAAAAAATT 180
 DB 121 GCAGGCTTCCTTAAACAGAACCCAGTGGTGATGTAATAGATTTGAAAAAATT 180
 QY 181 GAAGATCTTATTCATCTATGCAATTTGATGCTACTTATATACGGAAGATGTTTAC 240
 DB 181 GAAGATCTTATTCATCTATGCAATTTGATGCTACTTATATACGGAAGATGTTTAC 240
 QY 241 CCCAGTTGCAAGTAACAGCAATGAACTGCTTCTGAGATTTCAGATTATTTCACTT 300
 DB 241 CCCAGTTGCAAGTAACAGCAATGAACTGCTTCTGAGATTTCAGATTATTTCACTT 300
 QY 301 GAGTCGGAGATGCAATGATTCATGATGCTACTTATATACGGAAGATGTTTAC 360
 DB 301 GAGTCGGAGATGCAATGATTCATGATGCTACTTATATACGGAAGATGTTTAC 360
 QY 361 ACTTGTCTTCTAATGGGATGTAACAGATTCGATGCCAAGATGTGAGAACTGGAG 420
 DB 361 ACTTGTCTTCTAATGGGATGTAACAGATTCGATGCCAAGATGTGAGAACTGGAG 420
 QY 421 GAAAAAATATTAAAGATTTTTCAGAGATTGTTACATATTGTCCAAATGTTCACTAC 480
 DB 421 GAAAAAATATTAAAGATTTTTCAGAGATTGTTACATATTGTCCAAATGTTCACTAC 480
 QY 481 ACTTCTTGA 489
 DB 481 ACTTCTTGA 489

RESULT 7
 ARI25105 ARI25105 489 bp DNA linear PAT 16-MAY-2001
 LOCUS Sequence 2 from patent US 6177079.
 DEFINITION ARI25105
 ACCESSION ARI25105
 VERSION ARI25105.1 GI:14111167
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 489)
 AUTHORS Grabsstein,K.H., Pettit,D.K. and Paxton,R.J.
 TITLE Antagonists of Interleukin-15
 JOURNAL Patent: US 6177079-A 2 23-JAN-2001;
 FEATURES
 source location/Qualifiers
 1..489

BASE COUNT 159 a 79 c 95 g 156 t
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACCCATTTGAGAGATTTCCATCCAGTCTACTTGTTCATT 60
 DB 1 ATGAGATTTCGAACCCATTTGAGAGATTTCCATCCAGTCTACTTGTTCATT 60
 QY 61 CTAACAGCTATTTTCTAATCTAAGCTGCATTCATCTTCAATTTGGCTGTTCACT 120
 DB 61 CTAACAGCTATTTTCTAATCTAAGCTGCATTCATCTTCAATTTGGCTGTTCACT 120
 QY 121 GCAGGCTTCCTTAAACAGAACCCAGTGGTGATGTAATAGATTTGAAAAAATT 180
 DB 121 GCAGGCTTCCTTAAACAGAACCCAGTGGTGATGTAATAGATTTGAAAAAATT 180
 QY 181 GAAGATCTTATTCATCTATGCAATTTGATGCTACTTATATACGGAAGATGTTTAC 240
 DB 181 GAAGATCTTATTCATCTATGCAATTTGATGCTACTTATATACGGAAGATGTTTAC 240
 QY 241 CCCAGTTGCAAGTAACAGCAATGAACTGCTTCTGAGATTTCAGATTATTTCACTT 300
 DB 241 CCCAGTTGCAAGTAACAGCAATGAACTGCTTCTGAGATTTCAGATTATTTCACTT 300
 QY 301 GAGTCGGAGATGCAATGATTCATGATGCTACTTATATACGGAAGATGTTTAC 360
 DB 301 GAGTCGGAGATGCAATGATTCATGATGCTACTTATATACGGAAGATGTTTAC 360
 QY 361 ACTTGTCTTCTAATGGGATGTAACAGATTCGATGCCAAGATGTGAGAACTGGAG 420
 DB 361 ACTTGTCTTCTAATGGGATGTAACAGATTCGATGCCAAGATGTGAGAACTGGAG 420
 QY 421 GAAAAAATATTAAAGATTTTTCAGAGATTGTTACATATTGTCCAAATGTTCACTAC 480
 DB 421 GAAAAAATATTAAAGATTTTTCAGAGATTGTTACATATTGTCCAAATGTTCACTAC 480
 QY 481 ACTTCTTGA 489
 DB 481 ACTTCTTGA 489

RESULT 8
 AX006786 AX006786 489 bp DNA linear PAT 06-SEP-2000
 LOCUS Sequence 4 from Patent W00002582.
 DEFINITION AX006786
 ACCESSION AX006786
 VERSION AX006786.1 GI:9994822
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 489)
 AUTHORS Londel,M., Quarantino,S. and Majuri,L.
 TITLE Treatment of celliac disease with Interleukin-15 antagonists
 JOURNAL Patent: WO 0002582-A 4 20-JAN-2000;
 LONDEI MARCO (GB); QUARANTINO SONIA (GB); MATHILDA AND TERENCE
 KENNEDY I (GB); MAJURI LUGGI (IT)
 FEATURES
 source location/Qualifiers
 1..489
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 159 a 79 c 95 g 156 t
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;

Best Local Similarity	100.0%	Pred No. 1.2e-92:	Matches	489:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps	0:
QY	1	ATGAGAAATTTCCAAACACACATTTGAGAAATTTCCATCCAGCTGCTACTTGTCTTACTT	60									
Db	1	ATGAGAAATTTCCAAACACACATTTGAGAAATTTCCATCCAGCTGCTACTTGTCTTACTT	60									
QY	61	CTAACAAGTCATTTTCTAACTGAGCTGGCATTCTCAGTTTGGGCTGTTCACT	120									
Db	61	CTAACAAGTCATTTTCTAACTGAGCTGGCATTCTCAGTTTGGGCTGTTCACT	120									
QY	121	GCAGGCTTCCCTAAACAGAGACCACTGGGTGAATGTATTAAGTATTTGAAAAAAT	180									
Db	121	GCAGGCTTCCCTAAACAGAGACCACTGGGTGAATGTATTAAGTATTTGAAAAAAT	180									
QY	181	GAGATCTTATTCATCTATGCAATTTGATGCTACTTTATATACGAAAGTATGTTAC	240									
Db	181	GAGATCTTATTCATCTATGCAATTTGATGCTACTTTATATACGAAAGTATGTTAC	240									
QY	241	CCCAAGTTGCAAAATACAGCAATGAAGTGGCTTCTCTGGAGTTACAGTTATTTCACT	300									
Db	241	CCCAAGTTGCAAAATACAGCAATGAAGTGGCTTCTCTGGAGTTACAGTTATTTCACT	300									
QY	301	GAGTCGCGAGATGCAATATTCATGATATACAGTAAAGAAATCTGATCATCTACAGAAACAC	360									
Db	301	GAGTCGCGAGATGCAATATTCATGATATACAGTAAAGAAATCTGATCATCTACAGAAACAC	360									
QY	361	AGTTGTCTTCTTAATGCGAATGTAAACGAATCTGAGTACCAAGAAATGTAGAAACTGAG	420									
Db	361	AGTTGTCTTCTTAATGCGAATGTAAACGAATCTGAGTACCAAGAAATGTAGAAACTGAG	420									
QY	421	GAAAAAATATTTAAAGATTTTTCAGAGTTTGTACATATTTGCCAAATGTTTCATAC	480									
Db	421	GAAAAAATATTTAAAGATTTTTCAGAGTTTGTACATATTTGCCAAATGTTTCATAC	480									
QY	481	ACTTCTTGA	489									
Db	481	ACTTCTTGA	489									
RESULT	10											
LOCUS	125783		489 bp	DNA	linear							
DEFINITION	Sequence 4 from patent US 5552303.											
ACCESSION	125783											
VERSION	125783.1											
KEYWORDS												
SOURCE	Unknown.											
ORGANISM	Unknown.											
REFERENCE	1 (bases 1 to 489)											
AUTHORS	Grabstein, K., Anderson, D., Eisenman, J., Fung, V. and Rauch, C.											
TITLE	DNA encoding epithelium-derived T-cell factor											
JOURNAL	Patent: US 5552303-A 4 03-SEP-1996;											
FEATURES	Location/Qualifiers											
source	1..489											
BASE COUNT	159 a	79 c	95 g	156 t								
ORIGIN												
Query Match	100.0%:	Score 489:	DB 6:	Length 489:								
Best Local Similarity	100.0%:	Pred. No. 1.2e-										

QY 121 GCAGGGCTTCCTAAACAGAACCCCACTGGGTGATGTATAAGTATTGAAAAAATT 180
DB 121 GCAGGGCTTCCTAAACAGAACCCCACTGGGTGATGTATAAGTATTGAAAAAATT 180
QY 181 GAAGATCTTATCAATCTATGATGATGCTACTTTATATACGAAAGATGTTCC 240
DB 181 GAAGATCTTATCAATCTATGATGATGCTACTTTATATACGAAAGATGTTCC 240
QY 241 CCCAGTTGCAAGTAACAGCAATGAGTCTTCTCTGGAGTTTCAAGTTTTCAC 300
DB 241 CCCAGTTGCAAGTAACAGCAATGAGTCTTCTCTGGAGTTTCAAGTTTTCAC 300
QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAGTAATCTGATCCTTACCAAC 360
DB 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAGTAATCTGATCCTTACCAAC 360
QY 361 AGTTGTCTTCTTAATGGAGATGTACAGATCTGATCCTTACCAAGTCTGAG 420
DB 361 AGTTGTCTTCTTAATGGAGATGTACAGATCTGATCCTTACCAAGTCTGAG 420
QY 421 GAAAAAATTTAAGAAATTTTGCAGAGTTTGTACATTTGCCAAATGTCATC 480
DB 421 GAAAAAATTTAAGAAATTTTGCAGAGTTTGTACATTTGCCAAATGTCATC 480
QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 11
LOCUS 128849 489 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5574138.
ACCESSION 128849
VERSION 128849.1 GI:1819629
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Epithelium-derived T-cell factor
JOURNAL Patent: US 5574138-A 1 12-NOV-1996;
FEATURES
source 1..489
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 1,2e-92;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATTTTGAACACCATTTGAGATATTTCCATCCAGTGTACTTGTACTT 60
DB 1 ATGAGAATTTTGAACACCATTTGAGATATTTCCATCCAGTGTACTTGTACTT 60
QY 61 CTAAACAGTCAATTTCTACTGAAAGCTGGCATTCATGCTTCAATTTGGGCTGTT 120
DB 61 CTAAACAGTCAATTTCTACTGAAAGCTGGCATTCATGCTTCAATTTGGGCTGTT 120
QY 121 GCAGGGCTTCCTAAACAGAACCCCACTGGGTGATGTATAAGTATTGAAAAAATT 180
DB 121 GCAGGGCTTCCTAAACAGAACCCCACTGGGTGATGTATAAGTATTGAAAAAATT 180
QY 181 GAAGATCTTATCAATCTATGATGATGCTACTTTATATACGAAAGATGTTCC 240
DB 181 GAAGATCTTATCAATCTATGATGATGCTACTTTATATACGAAAGATGTTCC 240
QY 241 CCCAGTTGCAAGTAACAGCAATGAGTCTTCTCTGGAGTTTCAAGTTTTCAC 300
DB 241 CCCAGTTGCAAGTAACAGCAATGAGTCTTCTCTGGAGTTTCAAGTTTTCAC 300

QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAGTAATCTGATCCTTACCAAC 360
DB 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAGTAATCTGATCCTTACCAAC 360
QY 361 AGTTGTCTTCTTAATGGAGATGTACAGATCTGATCCTTACCAAGTCTGAG 420
DB 361 AGTTGTCTTCTTAATGGAGATGTACAGATCTGATCCTTACCAAGTCTGAG 420
QY 421 GAAAAAATTTAAGAAATTTTGCAGAGTTTGTACATTTGCCAAATGTCATC 480
DB 421 GAAAAAATTTAAGAAATTTTGCAGAGTTTGTACATTTGCCAAATGTCATC 480
QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 12
LOCUS 162692 489 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5660824.
ACCESSION 162692
VERSION 162692.1 GI:2480400
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Quinn,L.S. and Trout,A.B.
TITLE Muscle trophic factor
JOURNAL Patent: US 5660824-A 1 26-AUG-1997;
FEATURES
source 1..489
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 1,2e-92;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATTTTGAACACCATTTGAGATATTTCCATCCAGTGTACTTGTACTT 60
DB 1 ATGAGAATTTTGAACACCATTTGAGATATTTCCATCCAGTGTACTTGTACTT 60
QY 61 CTAAACAGTCAATTTCTACTGAAAGCTGGCATTCATGCTTCAATTTGGGCTGTT 120
DB 61 CTAAACAGTCAATTTCTACTGAAAGCTGGCATTCATGCTTCAATTTGGGCTGTT 120
QY 121 GCAGGGCTTCCTAAACAGAACCCCACTGGGTGATGTATAAGTATTGAAAAAATT 180
DB 121 GCAGGGCTTCCTAAACAGAACCCCACTGGGTGATGTATAAGTATTGAAAAAATT 180
QY 181 GAAGATCTTATCAATCTATGATGATGCTACTTTATATACGAAAGATGTTCC 240
DB 181 GAAGATCTTATCAATCTATGATGATGCTACTTTATATACGAAAGATGTTCC 240
QY 241 CCCAGTTGCAAGTAACAGCAATGAGTCTTCTCTGGAGTTTCAAGTTTTCAC 300
DB 241 CCCAGTTGCAAGTAACAGCAATGAGTCTTCTCTGGAGTTTCAAGTTTTCAC 300
QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAGTAATCTGATCCTTACCAAC 360
DB 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAGTAATCTGATCCTTACCAAC 360
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DB 361 AGTTGTCTTCTTAATGGAGATGTACAGATCTGATCCTTACCAAGTCTGAG 420
QY 421 GAAAAAATTTAAGAAATTTTGCAGAGTTTGTACATTTGCCAAATGTCATC 480
DB 421 GAAAAAATTTAAGAAATTTTGCAGAGTTTGTACATTTGCCAAATGTCATC 480

Db 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATGTCGCAAAATGTCATCAC 480
OY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 13
179219 179219 489 bp DNA linear PAT 10-JUN-1998
LOCUS Sequence 1 from patent US 5707616.
DEFINITION I79219
ACCESSION I79219
VERSION I79219.1 GI:3207509
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 489)
TITLE Grabstein, K.H., Anderson, D.M., Eisenman, J.R., Fung, Y. and Rauch, C.
METHOD for treating or preventing gastrointestinal disease with
epithelium-derived T-cell factor
JOURNAL Patent: US 5707616-A 13-JAN-1998;
FEATURES Location/Qualifiers
Source 1..489
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGAGAAATTTGCAACCAATTTGAGAGTATTTCCATCCAGTCTTGTACTT 60
Db 1 ATGAGAAATTTGCAACCAATTTGAGAGTATTTCCATCCAGTCTTGTACTT 60
OY 61 CTAAACAGTCATTTTCTAAGTCAAGCTGGCATTCATGCTTCTTATTTGGCGCTTTCAGT 120
Db 61 CTAAACAGTCATTTTCTAAGTCAAGCTGGCATTCATGCTTCTTATTTGGCGCTTTCAGT 120
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Db 121 GCAGGGCTTCCATAAAGCAAGCAAGTGGTGAATGTATTAAGTATTTGAAAAAAT 180
OY 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACGGAAGATGATGTCAC 240
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OY 361 AGTTTGTCTTCTAATGGAATGTACAGAAATCTGATGCAAAAGATGTAGAGAACTGGAG 420
Db 361 AGTTTGTCTTCTAATGGAATGTACAGAAATCTGATGCAAAAGATGTAGAGAACTGGAG 420
OY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTCATCAC 480
Db 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTCATCAC 480
OY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 14
ARI03280 ARI03280 1202 bp DNA linear PAT 14-FEB-2001
LOCUS

DEFINITION Sequence 11 from patent US 6087172.
ACCESSION ARI03280
VERSION ARI03280.1 GI:12814868
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS 1 (bases 1 to 1202)
TITLE Veerapanen, D., Hamanaka, S. and Nozawa, I.
JOURNAL Ribozymes targeted to human IL-15 mRNA
PATENT: US 6087172-A 11-11-JUL-2000;
FEATURES Location/Qualifiers
Source 1..1202
BASE COUNT 355 a 219 c 249 g 379 t
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 1202;
Best Local Similarity 100.0%; Pred. No. 9.4e-93;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGAGAAATTTGCAACCAATTTGAGAGTATTTCCATCCAGTCTTGTACTT 60
Db 317 ATGAGAAATTTGCAACCAATTTGAGAGTATTTCCATCCAGTCTTGTACTT 376
OY 61 CTAAACAGTCATTTTCTAAGTCAAGCTGGCATTCATGCTTCTTATTTGGCGCTTTCAGT 120
Db 377 CTAAACAGTCATTTTCTAAGTCAAGCTGGCATTCATGCTTCTTATTTGGCGCTTTCAGT 436
OY 121 GCAGGGCTTCCATAAAGCAAGCAAGTGGTGAATGTATTAAGTATTTGAAAAAAT 180
Db 437 GCAGGGCTTCCATAAAGCAAGCAAGTGGTGAATGTATTAAGTATTTGAAAAAAT 496
OY 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACGGAAGATGATGTCAC 240
Db 497 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACGGAAGATGATGTCAC 556
OY 241 CCCAGTTGCAAAATACAGCAATGAAGTCTTCTTCTTGAGATTAACAAGTATTTTCACTT 300
Db 557 CCCAGTTGCAAAATACAGCAATGAAGTCTTCTTCTTGAGATTAACAAGTATTTTCACTT 616
OY 301 GAGTCGGAGATGCAGATATTCATGATAGATGAAGAAATCTGATCATTCTAGCAAAACAC 360
Db 617 GAGTCGGAGATGCAGATATTCATGATAGATGAAGAAATCTGATCATTCTAGCAAAACAC 676
OY 361 AGTTTGTCTTCTAATGGAATGTACAGAAATCTGATGCAAAAGATGTAGAGAACTGGAG 420
Db 677 AGTTTGTCTTCTAATGGAATGTACAGAAATCTGATGCAAAAGATGTAGAGAACTGGAG 736
OY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTCATCAC 480
Db 737 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTCATCAC 796
OY 481 ACTTCTTGA 489
Db 797 ACTTCTTGA 805

RESULT 15
AX024715 AX024715 1202 bp DNA linear PAT 15-SEP-2000
LOCUS Sequence 1 from Patent W00028019.
DEFINITION AX024715
ACCESSION AX024715
VERSION AX024715.1 GI:10184794
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1202)
TITLE Doudevani, A. and Chaimovitz, C.
Antisense oligomer

JOURNAL

Patent: WO 0028019-A 1 18-MAY-2000;
MOR RESEARCH APPLIC LTD (IL) ; DOUDEVANI AMOS (IL) ; UNIV BEN
GURION (IL) ; CHAIMOVITZ CIDIO (IL)
Location/Qualifiers

FEATURES

source

1. 1202

/organism="Homo sapiens"

/db_xref="taxon:9606"

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 355 a 219 c 249 g 379 t
ORIGIN

Query Match

Best Local Similarity 100.0%; Score 489; DB 6; Length 1202;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTGCAACCAATTTGAGAGTATTTCCATCCAGTCTACTTGTGTTTACTT 60
DB 317 ATGAGATTTGCAACCAATTTGAGAGTATTTCCATCCAGTCTACTTGTGTTTACTT 376
QY 61 CTAACAGCTCATTTTCTAAGTGAAGCTGGCATGTCATGTCATTTGGGCTGTTTCACT 120
DB 377 CTAACAGCTCATTTTCTAAGTGAAGCTGGCATGTCATGTCATTTGGGCTGTTTCACT 436
QY 121 GCAGGGCTTCTTAACAGAGCAAGCACTGGGTGAATGTAATAGTATTTGAAAAAATT 180
DB 437 GCAGGGCTTCTTAACAGAGCAAGCACTGGGTGAATGTAATAGTATTTGAAAAAATT 496
QY 181 GAAGATCTTATTCATATGATATGATGCTACTTTATATACGAAAGTATGTTTCACT 240
DB 497 GAAGATCTTATTCATATGATATGATGCTACTTTATATACGAAAGTATGTTTCACT 556
QY 241 CCCAGTTGCAAGTAAAGCAATGAGTGGTCTTCTTGGAGTTTACAAAGTTATTTTCACTT 300
DB 557 CCCAGTTGCAAGTAAAGCAATGAGTGGTCTTCTTGGAGTTTACAAAGTTATTTTCACTT 616
QY 301 GAGTCCGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTAGCAAAACAC 360
DB 617 GAGTCCGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTAGCAAAACAC 676
QY 361 AGTTTGTCTTCTAATGGAGTGTACAGAACTGATGCAAAAGATGTGAGAACTGGAG 420
DB 677 AGTTTGTCTTCTAATGGAGTGTACAGAACTGATGCAAAAGATGTGAGAACTGGAG 736
QY 421 GAAAAAATTTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAATGTTTCACTCAG 480
DB 737 GAAAAAATTTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAATGTTTCACTCAG 796
QY 481 ACTTCTTGA 489
DB 797 ACTTCTTGA 805

Search completed: June 19, 2002, 01:32:22
Job time: 4950 sec

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 00:09:42 ; Search time 254.13 Seconds
(without alignments)
3303.707 Million cell updates/sec

Title: US-09-724-841-1
Perfect score: 489
Sequence: 1 ATGAGAAATTTCGAAACCA.....TGTCATCAACACTTCTTGA 489

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	489	100.0	489	16	AA00526
2	489	100.0	489	16	AA084584
3	489	100.0	489	17	AA049455
4	489	100.0	489	17	AA042243
5	489	100.0	489	17	AA036635
6	489	100.0	489	18	AA058404
7	489	100.0	489	19	AA023554
8	489	100.0	489	19	AA02873
9	489	100.0	489	20	AA029479

10	489	100.0	489	21	AA090032	Human interleukin-15
11	489	100.0	489	21	AA038244	Simian epithelium
12	489	100.0	489	22	AA014465	Human interleukin-15
13	489	100.0	489	22	AA057017	Simian ERF (SEF)
14	489	100.0	1202	20	AA056368	Human IL-15 DNA
15	489	100.0	1202	21	AA021342	Human low adenosin
16	489	100.0	1202	21	AA058044	Human interleukin-15
17	489	100.0	1202	21	AA055220	Human adenosine re
18	489	100.0	1202	21	AA028708	Human IL-15 cDNA
19	489	100.0	17904	21	AA021345	Human low adenosin
20	487.4	99.7	489	18	AA097227	Wild-type interlev
21	481	98.4	489	18	AA097228	Mutant interleukin
22	465	95.1	489	16	AA00524	Simian interleukin
23	465	95.1	489	16	AA084583	Simian IL-15 clone
24	465	95.1	489	17	AA049456	Human epithelium d
25	465	95.1	489	17	AA042242	Simian interleukin
26	465	95.1	489	17	AA036634	Human epithelium-d
27	465	95.1	489	19	AA02874	Human epithelium
28	465	95.1	489	20	AA029480	Simian interleukin
29	465	95.1	489	21	AA090031	Human ERF (HERF) p
30	465	95.1	489	21	AA038245	Human adenosine re
31	465	95.1	489	22	AA057018	Human low adenosin
32	385	78.7	17844	21	AA035223	Human adenosine re
33	378.4	77.4	1248	21	AA021341	Human interleukin
34	378.4	77.4	1248	21	AA035219	Human low adenosin
35	378.4	77.4	1248	21	AA021344	Human adenosine re
36	351.6	71.9	486	21	AA021344	Human interleukin
37	351.6	71.9	486	21	AA00522	Simian ERF (SEF)
38	345	70.6	345	16	AA057024	Simian interleukin
39	345	70.6	345	16	AA057024	Simian interleukin
40	325.8	66.6	345	16	AA00525	Human ERF (HERF) m
41	325.8	66.6	345	12	AA057025	Human low adenosin
42	141.6	29.0	14968	21	AA021343	Human adenosine re
43	141.6	29.0	14968	21	AA035221	Human IL-15 gene a
44	141.6	29.0	14968	22	AA014464	Human interleukin
45	141.6	29.0	14968	22	AA015838	Human interleukin

ALIGNMENTS

RESULT 1	
AA00526	AA00526 standard; cDNA; 489 BP.
ID	AA00526
XX	AA00526
AC	02-FEB-1996 (first entry)
XX	
DT	Human interleukin-15 precursor.
DE	Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.
XX	
KW	Homo sapiens.
OS	
XX	
FH	Key
FT	1..489
FT	Location/Qualifiers
FT	/*tag= a
FT	/note= "claimed"
FT	145..489
FT	/*tag= b
FT	/note= "claimed"
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PN	W09527722-A.
PD	19-OCT-1995.
XX	
PF	06-APR-1994; 94WO-US03793.
XX	
PR	06-APR-1994; 94WO-US03793.
XX	
PA	(IMM) IMMUNEX CORP.
XX	

PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 PI Rauch C;
 DR WPI: 1995-373556/48.
 DR P-PSDB: AAR83438.
 PT Isolated DNA encoding polypeptide with mammalian IL-15 activity - which
 PT stimulates proliferation and differentiation of T cells, used for
 PT treating carcinoma(s), melanomas, etc. and viral infections
 XX
 PS Claim 36: Page 28-29; 48pp; English.

CC A simian species of IL-15 (sIL-15) was purified and its AA
 CC sequence and cDNA sequence analysed (see AAR83309, AAR83436,
 CC AAT00524, AAT00525). Both the simian and the human ORFs encode
 CC a precursor polypeptide (AAR83436, AAR83438). The precursor
 CC polypeptides each comprise a 48-AA leader sequence and a sequence
 CC encoding mature simian or human IL-15 polypeptides. The active
 CC simian and human IL-15 polypeptides are disclosed in AAR83309 &
 CC AAR83310 respectively. The invention also comprises other mammalian
 CC IL-15, including human IL-15, that hybridise to probes defined by
 CC AAR83438. A plasmid contg. a recombinant clone of human IL-15
 CC cDNA was deposited with ATCC on Feb. 19 1993 under ATCC 69245.
 CC The deposit was named 141-hETF. AAR83435 is a mammalian mature
 CC IL-15 polypeptide. It is a generic sequence which encompasses both
 CC AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.
 XX
 XX Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 16; Length 489;
 Best Local Similarity 100.0%; Pred. No. 5.7e-117;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTCAAAACACATTTGAGAAGTATTTCCATCCAGTCTACTGTTACTT 60
 DB 1 atgagaatttcgaacaacacattgagaagatttcacatccagtcacttggttactt 60
 QY 61 CTAAAGATCATTTTCTTAAGTGAAGTGGCATTCATGCTCTTCTTGGGCTGTTCACT 120
 DB 61 ctaaacagtcattcttcaactgaagctggcatcattcattcttggctggttcaagt 120
 QY 121 GCAGGCTTCTTAAACAGAACGCACTGGTGAATGTAATGAAGTATTTGAAAAAAT 180
 DB 121 gcaggcttccttaaaacagaaagcgaactggtgaatgataagatttgaaaaaat 180
 QY 121 gcaaggcttccttaaaacagaaagcgaactggtgaatgataagatttgaaaaaat 180
 DB 121 gcaaggcttccttaaaacagaaagcgaactggtgaatgataagatttgaaaaaat 180
 QY 181 GAAGATCTTATTCATCTATGCATATGATGCTACTTTATATAGCGAAAGTGTTCAC 240
 DB 181 gaagatcttattcaatcattgcatatlgatgctactttatatacgaagaagtgttcac 240
 QY 241 CCCAGTTGCAAAAGTAACAGCAATGAAGTCTTCTTGGAGTTACAGTTATTTCACTT 300
 DB 241 cccagttgcaaaagtaacagcaatgaagcttcttcttggagttacaagttatttcactt 300
 QY 301 GAGTCGGAGATGCAAGATTTATCATATACAGTAAATCTGCATCATCTAGCAAAAC 360
 DB 301 gagtcggagatgcaagatTTTATCATATACAGTAAATCTGCATCATCTAGCAAAAC 360
 QY 361 agttgctctctcaatggaatgtaacagaatctggaagcaagaatctggaagcaatctggaag 420
 DB 361 agttgctctctcaatggaatgtaacagaatctggaagcaagaatctggaagcaatctggaag 420
 QY 421 GAAAAAATATTTAAAGATTTTTCAGAGTGTTCATATTTGCAAAATTTTCATCAAC 480
 DB 421 gaaaaaataataaagaatttctgcaagattctgacatattgcacaaatgattatcaaac 480
 QY 481 ACTTCTTGA 489
 DB 481 acttcttga 489

RESULT 2
 AA084584

ID AA084584 standard; cDNA; 489 BP.
 XX
 AC AA084584;
 XX
 DR 04-SEP-1995 (first entry)
 XX
 DE Human IL-15 clone 141.hETF.
 XX
 KM Interleukin-15; IL-15; hIL-15; T-cell growth factor;
 KM antitumor; virucide; ss.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 XX CDS 1..489
 XX FT /tag= a
 XX FT /product= IL-15 precursor
 XX FT sig_peptide 1..144
 XX FT mat_peptide 145..486
 XX FT /tag= b
 XX FT /tag= c
 XX FT /product= mature IL-15

XX ZA9402636-A.
 XX PD 28-DEC-1994.
 XX PF 18-APR-1994; 942A-0002636.
 XX PR 18-APR-1994; 942A-0002636.
 XX PA (IMMV) IMMUNEX CORP.
 XX PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 XX PI Rauch C;

XX WPI: 1995-082473/11.
 XX DR P-PSDB: AAR66927.
 XX PT New purified interleukin-15 - which induces T cell proliferation
 XX PT and differentiation, used for the treatment of tumours and viral
 XX PT infection
 XX PS Disclosure: Page 28-29; 47pp; English.

CC A sIL-15 probe was prepared from isolated simian interleukin-15
 CC cDNA and used to screen a cDNA library generated from the IMPLH
 CC cell line derived from human bone marrow stromal cells. Clone
 CC 141.hETF encoded human IL-15.
 XX

Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 16; Length 489;
 Best Local Similarity 100.0%; Pred. No. 5.7e-117;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTCAAAACACATTTGAGAAGTATTTCCATCCAGTCTACTGTTACTT 60
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 DB 121 gcaaggcttccttaaaacagaaagcgaactggtgaatgataagatttgaaaaaat 180
 QY 181 GAAGATCTTATTCATCTATGCATATGATGCTACTTTATATAGCGAAAGTGTTCAC 240
 DB 181 gaagatcttattcaatcattgcatatlgatgctactttatatacgaagaagtgttcac 240

OY 241 CCCAGTGCAGAACTACACAGCAATGAGTCTTCTCTGAGTTACAGTTATTCACCTT 300
 DB 241 cccagtgtaaaagtaacacgaatgaagtgcttctcttgagtgtaacagttatctactt 300
 OY 301 GAGTCCGAGATGACAGTATTCATGATACAGTAAATCTGATCTCAGCAAAACAC 360
 DB 301 gagtcgagatgacagatctatcatgatacagtaagaatctgatacctcgaacaacac 360
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 OY 481 ACTTCTTGA 489
 DB 481 acttcttga 489
 RESULT 3
 AAT49455
 ID AAT49455 standard; cDNA; 489 BP.
 AC AAT49455;
 XX 11-MAR-1997 (first entry)
 DE Simian epithelium derived T cell factor cDNA.
 XX
 KM SETF: African green monkey; CV1/EBNA cell; T-cell; B-cell;
 KM lymphocyte; proliferation; differentiation; gastrointestinal;
 KM HIV infection; human immunodeficiency virus; ss.
 XX
 OS Cercopithecus aethiops.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..489
 FT mat_peptide /*tag= a
 FT /*tag= b
 FT /product= SETF
 XX
 PN USS574138-A.
 PD 12-NOV-1996.
 XX
 PF 08-MAR-1993; 93US-0031399.
 XX
 PR 22-FEB-1995; 95US-0393305.
 PR 08-MAR-1993; 93US-0031399.
 PR 22-APR-1994; 94US-0233606.
 XX
 PA (IMMV) IMMUNEX CORP.
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 PI Rauch C;
 XX
 DR WPI: 1996-517923/51.
 DR P-PSDB: AAM09098 AND AAM09099.
 XX
 PT New epithelium derived T cell factor - induces proliferation of T
 PT and B cells; stimulates destruction of tumour and virus-infected
 PT cells and protects against toxicity, partic. for treating intestinal
 PT disease and HIV infection
 XX
 PS Claim 1; Fig 1; 35pp; English.
 CC The simian ETF (epithelium derived T cell factor) was isolated from
 CC African green monkey CV1/EBNA cell conditioned medium. The N-
 CC terminal sequence of the purified SETF was determined and then PCR
 CC primers were designed based on the sequence information. A 92 bp

CC Fragment was amplified from CV1/EBNA DNA and was used as a probe to
 CC screen a CV1/EBNA cDNA library for the full-length SETF coding
 CC sequence (i.e. the present sequence). Mature SETF induces
 CC proliferation and/or differentiation of precursor or mature T cells
 CC and is useful for promoting long-term in vitro culture of
 CC T-lymphocytes and T-cell lines. It is used for treating
 CC gastrointestinal diseases including peptic ulcer, colitis and
 CC malignancy and for treating HIV infection.
 XX
 SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;
 Query Match 100.0%; Score 489; DB 17; Length 489;
 Best Local Similarity 100.0%; Pred. No. 5.7e-117;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ATGAGAAATTTGCAACCAATTTGAGAGATTTCCATCCAGTCTCTGTGTTACTT 60
 DB 1 atgagaatttcgaacacacattgagaagatttccatccagtgctacttggttactt 60
 OY 61 CTAAACAGTATTTCTAAGTGAAGCTGATGATGATGATGATGATGATGATGATGAT 120
 DB 61 ctaaacagtcatttctaactgaagctgcatcagtcctcattcttggtgcttcaagt 120
 OY 121 GCAGGCTTCTCTAAGCAAGCCACTGGGTGAATGTAATGATGATGATGATGATGAT 180
 DB 121 gcagggttctcttaaacagaagccaaactgggtgagtgaatgaatgaatgaatgaat 180
 OY 181 GAAGATCTTATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 181 gaagatcttattcaatcattcagatgactgacttataatacgaagtgatgctcac 240
 OY 241 CCCAGTGCAGAACTACACAGCAATGAGTCTTCTCTGAGTTACAGTTATTCACCTT 300
 DB 241 cccagtgtaaaagtaacacgaatgaagtgcttctcttgagtgtaacagttatctactt 300
 OY 301 GAGTCCGAGATGACAGTATTCATGATACAGTAAATCTGATCTCAGCAAAACAC 360
 DB 301 gagtcgagatgacagatctatcatgatacagtaagaatcgcgaatgtaagtaagtaag 360
 OY 361 AGTTGCTCTTCAATGAGTAAACAGATCGATGCAAAAGATGTGAGCAACTGGAG 420
 DB 361 agttgctcttcaatgagtaagtaacagaaatcgcgaatgtaagtaagtaagtaag 420
 OY 421 GAAAAAATATTAAGCAATTTTGCAGATTTTGTACATTTTCCAAATGTCATCAAC 480
 DB 421 gaaaaaatatttaagaatlttgcagagtttgcatacatgtgccaaatgttccatcaac 480
 OY 481 ACTTCTTGA 489
 DB 481 acttcttga 489
 RESULT 4
 AAT42243
 ID AAT42243 standard; DNA; 489 BP.
 AC AAT42243;
 XX
 DT 05-FEB-1997 (first entry)
 XX
 DE Human epithelium-derived T cell factor gene.
 XX
 KM Epithelium-derived T-cell factor; simian; human; culture; proliferation;
 KM epithelial cell; differentiation; T-lymphocyte; African green monkey;
 KM primer; PCR; polymerase chain reaction; amplification; probe; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT sig_peptide 1..144
 FT /*tag= a
 FT mat_peptide 145..486

```

FT  XX  /tag= b
XX  PN  US5552303-A.
XX  PD  03-SEP-1996.
XX  PF  08-MAR-1993; 93US-0031399.
XX  PR  08-MAR-1993; 93US-0031399.
XX  PA  (IMMUNEX CORP.
PI  Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;
XX  WPI: 1996-412063/41.
DR  P-PSDB; AAM07255.
XX  PT  New isolated simian and human epithelium-derived T-cell factors -
XX  PT  which stimulate the proliferation and/or differentiation of
XX  PT  T-lymphocytes and T-cell lines
XX  PS  Claim 21; Column 23-24; 22pp; English.
XX  CC  This is the nucleotide sequence encoding a human epithelium-derived
XX  CC  T-cell factor (EMF). The gene was obtained using a 1.37 kb fragment of
XX  CC  the corresp. African green monkey gene (AAT4242) as a probe to screen a
XX  CC  cDNA library constructed from RNA derived from the IM7H cell line.
XX  CC  This cell line is derived by stable transformation of a human bone
XX  CC  marrow stromal cell culture with pSVneo. From a pool of about 1000 cDNA
XX  CC  clones, one clone 141.bTF contained this sequence. EMF is a protein of
XX  CC  15-17 kD which is expressed by epithelial cells and stimulates
XX  CC  proliferation and/or differentiation of precursor and/or mature T cells.
XX  CC  The protein is therefore useful for promoting long term in vivo culture
XX  CC  of T-lymphocytes and T-cell lines.
SQ  Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other:

Query Match 100.0%; Score 489; DB 17; Length 489;
Best Local Similarity 100.0%; Pred. No. 5,7e-117;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY  481 ACTTCCTGA 489
DB  481 actctctga 489

RESULT 5
AAT36635
ID  AAT36635 standard; cDNA; 489 BP.
XX
AC  AAT36635;
XX
DT  17-NOV-1996 (first entry)
XX
DE  Human Interleukin-15 cDNA.
XX
KM  Interleukin-15; antagonist; mutein; graft versus host disease;
XX  allograft; T-cell growth factor; ss.
XX
OS  Homo sapiens.
XX
PN  WO9626274-A1.
XX
PD  29-AUG-1996.
XX
PF  21-FEB-1996; 96WO-US02520.
XX
PR  22-FEB-1995; 95US-0392317.
XX
PA  (IMMUNEX CORP.
XX
PI  Grabstein KH, Paxton RJ, Pettit DK;
XX  WPI: 1996-402367/40.
XX  P-PSDB; AAR98527.
XX
PT  Antagonists of Interleukin-15 - are used to treat patients having
PT  symptoms of graft-versus-host disease and for prolonging allo-graft
PT  survival
XX
PS  Disclosure: Page 25; 32pp; English.
XX
CC  A cDNA clone (AAT36635) codes for human Interleukin-15 (IL-15)
CC  (AAR98527), a T-cell growth factor. Mutelins of human IL-15 or
CC  simian IL-15 (see also AAR98526) are useful as antagonists of IL-15
CC  and can be prep. by PCR-mediated mutagenesis of the encoding
CC  sequences. Preferred mutelins have amino acid substitutions at
CC  Asp56 and/or Glu156 of the IL-15 protein that prevent signal
CC  transduction. They are useful for treating graft-versus-host
CC  disease and for prolonging allograft survival.
SQ  Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other:

Query Match 100.0%; Score 489; DB 17; Length 489;
Best Local Similarity 100.0%; Pred. No. 5,7e-117;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


PR 22-APR-1994; 94US-0233606.
 XX 22-FEB-1995; 95US-0393305.
 PA (IMV) IMMUNEX CORP.
 XX
 PI Grabstein KH, Widmer MB;
 XX
 XX WPI, 1998-285678/25.
 DR P-PSDB; AAW53878.
 XX

PT Use of Interleukin-15 - to enhance immunogenicity of a vaccine
 XX

PS Disclosure: Column 5-6; 5pp; English.
 XX

CC This sequence encodes human interleukin-15 (IL-15), which can be used in
 CC the vaccine of the invention. The vaccine composition comprises an
 CC immunogenic amount of a vaccine antigen (Ag) and an
 CC immunogenicity-augmenting amount of IL-15. The composition is useful for
 CC enhancing the immunogenicity of a vaccine. The cytokine IL-15 is a potent
 CC T and B cell growth factor. It causes proliferation and differentiation
 CC of these cells and augments T cell mediated immune responses. The vaccine
 CC composition can sufficiently elicit an immune response without being
 CC deleterious to the recipient, especially when using pathogenically
 CC deficient antigens. Some vaccines do not elicit a strong immune response
 CC and cannot provide sufficient protection on further exposure to the
 CC antigen.
 CC
 XX
 XX

Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 19; Length 489;
 Best Local Similarity: 100.0%; Pred. No. 5,7e-117;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAAACACATTGAGAGATTTCATCCAGTGGTACTGTTACTT 60
 DB 1 atgagaatttcgaaacacattgagaagatttcacccagtgctacttggttactt 60
 QY 61 CTAAACAGTCAATTTCTTACTGAGAGCTGGCATTCCTTCTTCAATTTGGCGTGTTCAGT 120
 DB 61 ctaaacagtcatttcttaactgaagctgcatcctcattcctcatttggtcgttccagt 120
 QY 121 GCAGGGCTTCCTAAACAGACCCACTGGGTGATGTAATTAAGTATTGAAAAAATT 180
 DB 121 gcagggttccttaaacagacccactgggtgatgtaattaaagtattgaaaaaatt 180
 QY 181 GAAGATCTTATTCATATCATATGATGATGCTACTTATATACGAAAGATGTTTAC 240
 DB 181 gaagatcttattcatatcatatgcatattgacttacttataatcgaagaagatgttcaac 240
 QY 241 CCCACTTGCAGAAAGTACGCAATGAAGTCTTCTTCTTGGAGTTACAAAGTTATTTGACTT 300
 DB 241 cccacttgcagaaagtacgcaatgaagcttcttctctctgtgagttacaagttattcactt 300
 QY 301 GAGTCGCGAGATGCAAGTATCATGATGATGATGATAAATCGATCATCTGCAAAACAC 360
 DB 301 gagtcgcgagatgcaagatgcatgattgataaattcgatcatctgcaaaacac 360
 QY 361 AGTTGCTTCTTAATGGGAATGTAAAGAAATCTGATGCAAAAGATGTAGAGACTGGAG 420
 DB 361 agttgcttcttaattgggaatgtaaagaaatctgatgcaaaagatgtgagaaactggag 420
 QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAAGTTTATCAAC 480
 DB 421 gaaaaaataatlaaagaattttgcagagtttgtacatattgtccaaatgtcatcaaac 480
 QY 481 ACTTCTTGA 489
 DB 481 acttcttga 489

RESULT 8
 AAV02873

ID AAV02873 standard; DNA; 489 BP.

XX AAV02873;

AC 08-MAY-1998 (first entry)

DT Simian epithelium derived T-cell factor DNA.

DE Epithelium derived T-cell factor; ERF; simian; gastrointestinal disease;

KW B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;

KW treatment; prevention; ss.

OS Simian.

FT Key Location/Qualifiers

FT CDS 1..489

FT sig_peptide /*tag= a

FT mat_peptide /*tag= b

FT /*tag= C

FT /product= ERF

FT /note= "Epithelium-derived T-cell factor"

XX US5707616-A.

XX 13-JAN-1998.

XX 04-OCT-1996; 96US-0726817.

XX 22-FEB-1995; 95US-0393305.

XX 08-MAR-1993; 93US-0031399.

XX 22-APR-1994; 94US-0233606.

XX (IMV) IMMUNEX CORP.

XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;

XX Rauch C;

XX WPI: 1998-100295/09.

XX P-PSDB; AAW39185.

XX Claim 1C; Column 35-36; 34pp; English.

XX This sequence encodes a simian epithelium-derived T-cell factor (ERF)

XX which is used in a method for treating or preventing gastrointestinal

XX disease. These polypeptides have particular application in the treatment

XX of gastrointestinal disorders associated with disruption of the

XX gastrointestinal epithelium or villi such as chemotherapy- and

XX ulcer disease, gastroenteritis and colitis, villus atrophic disorders,

XX malignancy and inflammatory bowel disease. ERF polypeptides may also be

XX useful in the treatment of human immunodeficiency virus (HIV) and

XX HIV-associated disease due to their ability to stimulate CD4+ and CD8+

XX cells. Biologically active ERF may be used to treat a variety of other

XX diseases or conditions where T-cell or B cell stimulation is desired.

SO Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 19; Length 489;
 Best Local Similarity: 100.0%; Pred. No. 5,7e-117;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAAACACATTGAGAGATTTCATCCAGTGGTACTGTTACTT 60
 DB 1 atgagaatttcgaaacacattgagaagatttcacccagtgctacttggttactt 60
 QY 61 CTAAACAGTCAATTTCTTACTGAGAGCTGGCATTCCTTCTTCAATTTGGCGTGTTCAGT 120
 DB 1 ctaaacagtcatttcttaactgaagctgcatcctcattcctcatttggtcgttccagt 120

Db 61 ctaaacagtcatttcttaactgaagctgcatcattgcttcaatttggcgttccagt 120
 QY 121 GCAGGGCTTCTTAAACAGAACCACTGGTGAATGTAATGATTGAAAAAATT 180
 Db 121 gagggtcttcttaaacagaagcaacggtggaatgtaaatgatttgaaaaaatt 180
 QY 181 GAAGATCTTATTCATCTATGATATGATGCTACTTTATATACGGAAGTATGTCAC 240
 Db 181 gaagatcttattcaactatcatgatacttgaacttatacagaaagtatgttcac 240
 QY 241 CCCAGTGTCAAGTAAACAGCAATGAGTCTTCTCTTGGAGTTTCAATATTTCACAT 300
 Db 241 cccagtgtaaaagtaacagcaatgaagcttcttcccttggaattacaagtatttccact 300
 QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTTACCAACAC 360
 Db 301 gagtcggagatgcaagatctatcatgatacagtagaaatctgatacctcagaacaacac 360
 QY 361 AGTTGTCTTCTAATGCAATGTAACAGAACTGCAATGCAAGAAATGAGAACTGAG 420
 Db 361 agttgtcttcttaaatgcaatgttaacagaaatctgagtaaaagaaatgtaagaaactgag 420
 QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTCAATAC 480
 Db 421 gaaaaaataataaagaattttgcagagtttgtacatattgtccaaatgttcaatcac 480
 QY 481 ACTTCTTGA 489
 Db 481 acttcttga 489
 RESULT 9
 AA29479
 ID AA29479 standard; DNA; 489 BP.
 AC AA29479;
 XX 10-JUN-1999 (first entry)
 DE Simian epithelium-derived T-cell factor (ETF) encoding DNA.
 XX Epithelium-derived T-cell factor; ETF; immunoassay; enteritis; ulcer;
 KW T cell proliferation; gastrointestinal disease; mucositis; colitis;
 KW gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease;
 KW human immune deficiency virus; tumour; simian; ss.
 OS Mammalia.
 XX
 PN US5892001-A.
 XX
 PD 06-APR-1999.
 XX
 PF 04-OCT-1996; 9605-0725969.
 XX
 PR 22-FEB-1995; 9505-0393305.
 PR 08-MAR-1993; 9305-0031399.
 PR 22-APR-1994; 9405-0233606.
 PR 04-OCT-1996; 9605-0725969.
 XX
 PA (IMNV) IMMUNEX CORP.
 XX
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 PI Rauch C;
 DR WPI; 1999-253930/21.
 DR P-PSDB; AAY03756, AAY03757.
 XX
 PT Antibodies specific for epithelium-derived T-cell growth factor
 XX
 PS Claim 1; Columns 35-36; 34pp; English.
 CC The invention relates to an isolated antibody that binds specifically to
 CC a simian or human epithelium-derived T-cell factor (ETF) polypeptide. The

CC antibodies are used, optionally when immobilized or labeled, to detect
 CC and quantify ETF in standard immunoassays. They may also be used as
 CC diagnostic and therapeutic agents, e.g. when conjugated to toxins (or
 CC their precursors) or radionuclides. ETF induces proliferation and/or
 CC differentiation of T cells (or their precursors), e.g. for use in
 CC establishing long term in vitro cultures; and is also used to treat
 CC gastrointestinal disease (e.g. enteritis or mucositis induced by
 CC chemotherapy or radiation, peptic ulcer, gastroenteritis, colitis,
 CC villus atrophy, malignancy and inflammatory bowel disease), to treat
 CC human immune deficiency virus infection or associated disease, or
 CC generally in any situation requiring stimulation of T or B cell
 CC proliferation, secretion of immunoglobulins or certain cytokines,
 CC increased anti-infection disease immunity, induction of T-cell lytic
 CC activity or increased destruction of tumour or virus-infected cells. The
 CC present sequence represents a DNA encoding a simian ETF precursor
 CC polypeptide sequence.
 SO Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;
 Query Match 100.0%; Score 489; DB 20; Length 489;
 Best Local Similarity 100.0%; Pred. No. 5.7e-117;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAGAAATTCGAAACACATTTGAGAAATTTCCATCCAGTGTCTTGTCTTACTT 60
 Db 1 atgagaatttcgaaacacatttgagaagtattccatccagtgctacttggttactt 60
 QY 61 CTAAACAGTCATTTTCTTAACTGAAAGCTGGCAATGATGCTTCAATTTTGGCTTTCACT 120
 Db 61 ctaaacagtcatttcttaactgaagctgcatcattgcttcaatttggcgttccagt 120
 QY 121 GCAGGGCTTCTTAAACAGAACCACTGGTGAATGTAATGATTGAAAAAATT 180
 Db 121 gagggtcttcttaaacagaagcaacggtggaatgtaaatgatttgaaaaaatt 180
 QY 181 GAAGATCTTATTCATCTATGATATGATGCTACTTTATATACGGAAGTATGTCAC 240
 Db 181 gaagatcttattcaactatcatgatacttgaacttatacagaaagtatgttcac 240
 QY 241 CCCAGTGTCAAGTAAACAGCAATGAGTCTTCTCTTGGAGTTTCAATATTTCACAT 300
 Db 241 cccagtgtaaaagtaacagcaatgaagcttcttcccttggaattacaagtatttccact 300
 QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTTACCAACAC 360
 Db 301 gagtcggagatgcaagatctatcatgatacagtagaaatctgatacctcagaacaacac 360
 QY 361 AGTTGTCTTCTAATGCAATGTAACAGAACTGCAATGCAAGAAATGAGAACTGAG 420
 Db 361 agttgtcttcttaaatgcaatgttaacagaaatctgagtaaaagaaatgtaagaaactgag 420
 QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTCAATAC 480
 Db 421 gaaaaaataataaagaattttgcagagtttgtacatattgtccaaatgttcaatcac 480
 QY 481 ACTTCTTGA 489
 Db 481 acttcttga 489
 RESULT 10
 AA290032
 ID AA290032 standard; cDNA; 489 BP.
 AC AA290032;
 XX
 XX 09-MAY-2000 (first entry)
 DE Human interleukin-15 (IL-15) nucleotide sequence.
 XX
 PS Interleukin-15; IL-15; antagonist; irritable bowel disease; IBD;
 KW celiac disease; treatment; human; ss.

XX Homo sapiens.
 XX MO200002582-A2.
 XX 20-JAN-2000.
 XX 09-JUL-1999; 99WO-GB02201.
 XX 10-JUL-1998; 98GB-0014892.
 XX (KENN-) KENNEDY INST RHEUMATOLOGY MATHILDA & TER.
 XX Londer M, Quaratino S, Mairul L;
 XX WPI: 2000-171080/15.
 XX P-PSDB: AAY78595.
 XX Use of antagonists of Interleukin-15 for treating an inflammatory bowel
 XX disease, particularly celiac disease
 XX Disclosure: Page 70; 70pp; English.

CC This sequence represents the human Interleukin 15 (IL-15) nucleotide
 CC sequence. The IL-15 nucleotide sequence and the protein encoded by it can
 CC be used to determine and create antagonists of IL-15. An antagonist of
 CC IL-15 can be used for treating an inflammatory bowel disease (IBD). The
 CC invention relates to the treatment of celiac disease using IL-15
 CC antagonists. The antagonists are preferably mutants of IL-15, antibodies
 CC against IL-15 or IL-15 molecules bound to chemical groups that interfere
 CC with the ability of IL-15 to effect a signal transduction through either
 CC the alpha or the gamma subunit of the IL-15 receptor complex. The IL-15
 CC antagonists of the invention can be used to treat irritable bow disease
 CC especially celiac disease.

Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other:

Query Match 100.0%; Score 489; DB 21; Length 489;
 Best Local Similarity 100.0%; Pred. No. 5,7e-117;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACACATTTGGAAGTATTTCCATCCAGTGTCTGTTTACTT 60
 DB 1 atgagaatttcgaaacccacattggaagatttccaccagtgctacttgytttactt 60
 QY 61 CTAAACAGTCAATTTCTACTGAGCACTGCAATTCATGCTCTCATTTGGCGTTCAGT 120
 DB 61 ctaaacagtcatttcttaactgaagctggtcctcctcattcttggcgttcagtc 120
 QY 121 GCAGGCTTCTTAACAGAACCACTGGGTGAATGTAATAGTATTGAAAAAATT 180
 DB 121 gcaggcttcttaaacaggaagccacacgggtgaaatgaatgaatttgaaaaaatt 180
 QY 181 GAACATCTTATTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 181 gaacatcttattcaatcattgacatgacatgacatgacatgacatgacatgacatgac 240
 QY 241 CCCAGTTGCAAGTAAACAGCAATGAGTCTTCTCTGAGATTACAGTATTTCACTT 300
 DB 241 cccagttgcaagtaaacgcaatgagtgcttctcttgsggtacaaatgatttcaactt 300
 QY 301 GAGTCCGGAAGATGCAAGTATTCATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 301 gagtcggagatgcaagatcattgacatgacatgacatgacatgacatgacatgacatgac 360
 QY 361 AGTTGCTTCTTAATGGAATGTAACAGAAATCTGATGCAAGAAATGAGAACTGTGAG 420
 DB 361 agttgcttcttaattggaatgtaacagaaatctgacagaaatgtaagaaatgtaagaaat 420
 QY 421 GAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTTGCCAAATGTCATCAAC 480
 DB 421 gaaaaaataatlaagaatttttcagagtttgcagagtttgcagagtttgcagagtttgcagag 480

QY 481 ACTTCTTGA 489
 DB 481 acttcttga 489

RESULT 11
 AA238244
 ID AA238244 standard; cDNA; 489 BP.
 AC AA238244;
 XX 09-FEB-2000 (first entry)

DE Simian epithelium-derived T-cell factor (ETF) cDNA.
 XX
 KW ETF; epithelium-derived T-cell factor; T-cell; T-lymphocyte;
 KW proliferation; differentiation; growth factor; precursor; mature; CD4+;
 KW CD8+; gastrointestinal; epithelium; cell culture; treatment; HIV;
 KW gastrointestinal disease; gastroenteritis; colitis;
 KW inflammatory bowel disease; villus atrophic disorder; enteritis;
 KW chemotherapy; radiotherapy; gut toxicity; cancer; side effect;
 KW tolerated dose; ss.

OS Mammalia.

Key Location/Qualifiers

FT CDS 1..489

FT /tag- a

FT /product= "Simian ETF precursor protein (AA238244)"

FT sig_peptide 1..144

FT /tag- b

FT mat_peptide 145..489

FT /tag- c

FT /product= "Mature simian ETF (AA238244)"

US5985262-A.

16-NOV-1999.

03-FEB-1997; 97US-0794524.

22-FEB-1995; 95US-0393305.

04-OCT-1996; 96US-0726817.

08-MAR-1993; 93US-0031399.

22-APR-1994; 94US-0233606.

(IMV) IMMUNEX CORP.

Rauch C, Fung V, Eisenman JR, Grabstein KH, Anderson DM;
 WPI: 2000-022267/02.
 P-PSDB: AAY52308, AAY52309.

Claim 1; Columns 35-36; 33pp; English.

This sequence represents simian epithelium-derived T-cell factor (ETF)
 cDNA. ETF is a previously unidentified T-cell growth factor which
 stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to proliferate
 and differentiate. It also promotes proliferation of the gastrointestinal
 epithelium. The protein can be used to promote long-term in vitro culture
 of T-lymphocytes and T-cell lines. ETF can be used for treating HIV
 infection, HIV-associated diseases, and other diseases or conditions
 where stimulation of T-cell proliferation would be desirable e.g., it
 could be used to augment the destruction of tumour cells or virally-
 infected cells. ETF may also be used to treat or prevent gastrointestinal
 disease, including chemotherapy and radiotherapy associated enteritis,
 gastroenteritis, colitis, inflammatory bowel disease and villus atrophic
 disorders. Chemotherapy and radiotherapy associated enteritis (gut
 toxicity) results in bleeding and sepsis due to gastrointestinal flora

CC entering the blood, and thus can limit the dosage of therapeutic agent
CC administered to a cancer patient. Eff may therefore be used to increase
CC the tolerated doses radiotherapy and chemotherapy.
XX
XX
SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 21; Length 489;
Best Local Similarity 100.0%; Pred. No. 5.7e-117;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTTGGAACCACTTTGAGAGATTTCCATCCAGTCTACTGTGTACTT 60
DB 1 atgagaatttcgaaccacatttgagaagatttcattccagtcactcttgtaactt 60
QY 61 CTAACAGCTATTTCTCAATGAGTGGATTCATGCTTTCATTTTGGCTGTTCAGT 120
DB 61 ctacaacagtcattcttcaaccagcctgcatcactgcttcttcttggcgttccagt 120
QY 121 GCAGGCTTCTTAAACAGACCACTGGGTGAATGTAATAGTGAATTTGAAAAAATT 180
DB 121 gcagggcttcttaaaacagagccaactgggtgaatgtaataagtgattgaaaaaatt 180
QY 181 GAAGATCTTATTCATATGCAATATGATGCTTCTTATATACGGAAGGATGTTTAC 240
DB 181 gaagatcttattcaattcatatgcatatgacttatacaggaagtgatgcttcaac 240
QY 241 CCCAGTTGCAAGTAAACAGCAATGAGTGGCTTCTTTCGATTAAGTATTTTCACTT 300
DB 241 cccagttgcaagaagtaacagcaatgagtgagtgcttcttcttgggttaacagtttcaact 300
QY 301 GAGTCCGAGATGCAAGTATTCATGATACATAGTAAATTCGATTCCTTAGCAAAACAC 360
DB 301 gagtcggagagtgcaagatcattcagatcagtagaataatcgcattcctcagcaaacac 360
QY 361 AGTTTGTCTTCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 420
DB 361 agtttgtcttcaatgggaatggaatggaatggaatggaatggaatggaatggaatgga 420
QY 421 GAAAAAATATTAAGAAATTTTTCGAGAGTTTGTACATATTTGCCAAATGTTCAATC 480
DB 421 gaaaaaataataaagaatttttgcagaggttttgacatattgtccaaatgttccatcac 480
QY 481 ACTTCTTGA 489
DB 481 acttcttga 489

RESULT 12
AADI4465 standard; DNA; 489 BP.
ID AADI4465;
AC AADI4465;
XX
XX
DT 15-NOV-2001 (first entry)
DE Human interleukin 15 (IL-15) DNA coding sequence.
XX
XX
KW Human; interleukin 15; IL-15; gene therapy; chromosome 4q31; infection;
KW drug screening; anthropological lineage; paternity testing; HIV;
KW Human immunodeficiency Virus; forensic application; T-cell leukemia; ds.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 1..489
FT /tag= a
FT /product= "Human IL-15 protein"
XX
XX
PD WO200158914-A2.
XX
XX 16-AUG-2001.

PF 08-FEB-2001; 2001WO-US04130.
XX
XX 08-FEB-2000; 2000US-0181059.
PR
XX
XX (GENA-) GENAISANCE PHARM INC.
XX
XX
PI Anastasio AE, Chew A, Denton RR, Nandabalan K, Stephens JC;
XX
XX WPI, 2001-522460/57.
DR P-PSDB; AAE08576.
XX

PT Novel polynucleotides comprising one of IL, PSI-PSII, single nucleotide
PT polymorphisms in human interleukin-15 gene, and useful for treating
PT disorders affected by expression of function of interleukin-15 isogene
PT
PS Disclosure; Fig 2; 78pp; English.
XX
XX

CC The present sequence is human interleukin-15 (IL-15) DNA coding sequence
CC located on chromosome 4q31. The polymorphic variants of IL-15 genes are
CC useful for studying the expression and function of IL-15 and expressing
CC IL-15 protein for use in screening for candidate drugs to treat diseases
CC related to IL-15 activity. Genotyping or haplotyping an individual at the
CC novel IL-15 polymorphic sites are useful for studying population
CC diversity, anthropological lineage, the significance of diversity and
CC lineage of the phenotypic level, paternity testing, forensic applications
CC and for identifying associations between IL-15 genetic variation and a
CC trait such as level of drug response or susceptibility to disease.
CC Identifying an association between a genotype or haplotype and a trait,
CC identifying an association between diagnostic tests and therapeutic treatments for
CC infections, human immunodeficiency virus and T-cell leukemia. The
CC identification of an association between a clinical response and a
CC genotype or haplotype (or haplotype pair) for the IL-15 gene may be the
CC basis for designing a diagnostic method to determine those individuals
CC who will or will not respond to the treatment, or alternatively, will
CC respond at a lower level and thus may require more treatment, i.e. a
CC greater dose of a drug. The genotyping or haplotyping methods are also
CC useful for developing drugs targeting IL-15. The genotyping and
CC haplotyping methods are also useful in designing clinical trials. IL-15
CC DNA is useful for therapeutic purposes for treating disorders affected
CC by expression of function of novel IL-15 isogene and also in gene
CC therapy. Expression of an IL-15 isogene may be turned off by transforming
CC a targeted organ, tissue or cell population of an expression vector
CC that expresses high levels of untranslatable mRNA for the isogene.
XX
XX
SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 22; Length 489;
Best Local Similarity 100.0%; Pred. No. 5.7e-117;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTTGGAACCACTTTGAGAGATTTCCATCCAGTCTACTGTGTACTT 60
DB 1 atgagaatttcgaaccacatttgagaagatttcattccacagtcactcttgtaactt 60
QY 61 CTAACAGCTATTTCTCAATGAGTGGATTCATGCTTTCATTTTGGCTGTTCAGT 120
DB 61 ctacaacagtcattcttcaaccagcctgcatcactgcttcttcttggcgttccagt 120
QY 121 GCAGGCTTCTTAAACAGACCACTGGGTGAATGTAATAGTGAATTTGAAAAAATT 180
DB 121 gcagggcttcttaaaacagagccaactgggtgaatgtaataagtgattgaaaaaatt 180
QY 181 GAAGATCTTATTCATATGCAATATGATGCTTCTTATATACGGAAGGATGTTTAC 240
DB 181 gaagatcttattcaattcatatgcatatgacttatacaggaagtgatgcttcaac 240
QY 241 CCCAGTTGCAAGTAAACAGCAATGAGTGGCTTCTTTCGATTAAGTGAATTTTCACTT 300
DB 241 cccagttgcaagaagtaacagcaatgagtgcttcttcttgggttaacagtttccactt 300
QY 301 GAGTCCGAGATGCAAGTATTCATGATACATAGTAAATTCGATTCCTTAGCAAAACAC 360

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|||||
Db 301 ggtccgagatcgatcatcatcagagaatctgatatctctgcaaacac 360
Oy 361 ACTTGTCTCTTAATGGGAATTCACAGAACTGTCACAAAGATGTGAGCACTGGAG 420
Db 361 agttgtctctcaatgggaatgtacacagatctgagtcagaagtgtggaactgag 420
Oy 421 GAAAAAATATTAAAGAAATTTTTCAGAGTTTGTACATATTGTCCAAAGTTCATCAAC 480
Db 421 gaaaaaataataagaatttttgagaggtttgtacatatgtccaaatgtcatcac 480
Oy 481 ACTCTTGA 489
Db 481 actctctga 489

```

RESULT 13
AAFS7017
ID AAF57017 standard; cDNA: 489 BP.

XX AAF57017;

DT 14-MAY-2001 (first entry)

DE Simian ETF (SETF) polypeptide encoding cDNA.

KW Epithelium-derived T-cell factor; ETF; simian; human; enteritis;

KM gastrointestinal disease; mucositis; peptic ulcer; cytostatic;

KW villus atrophic disorder; inflammatory bowel disease; antinflammatory;

XX anti-HIV, antiviral; T-lymphocyte stimulator; ss.

OS Mammalia.

XX Key

FT CDS

FT Location/Qualifiers

FT 1..489

FT /*tag- a

FT /product- "SETF"

FT 1..144

FT sig-peptide

FT /*tag- b

FT 145..486

FT mat-peptide

FT /*tag- c

FT /note- "specifically claimed (see AAB62013)"

XX US6184359-B1.

XX 06-FEB-2001.

XX 09-NOV-1998; 98US-0189193.

XX 22-FEB-1995; 95US-0393305.

XX 04-OCT-1996; 96US-0725969.

XX 08-MAR-1993; 93US-0031399.

XX 22-APR-1994; 94US-0233606.

XX (IMMUNEX CORP.

XX Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;

XX WPI: 2001-217801/22.

XX P-PSDB: AAB62012, AAB62013.

XX New antibodies that specifically binds epithelium-derived T-cell factor

XX polypeptide useful for e.g. treating or preventing gastrointestinal

XX diseases, HIV and HIV-associated diseases, augmenting destruction of

XX tumour cells

XX Claim 1: Column 35-36; 35pp; English.

XX The invention relates to simian and human epithelium-derived T-cell

XX factor (ETF) polypeptides. Antibodies that specifically bind to the ETF

XX polypeptides are used for treating or preventing gastrointestinal

XX diseases, such as chemotherapy and radiation therapy-induced enteritis

XX and mucositis, peptic ulcer disease, villus atrophic disorders and

CC inflammatory bowel disease; for increasing tolerated doses for radiation
CC therapy and chemotherapy agents which are limited by gastrointestinal
CC toxicity; and for treating HIV and HIV-associated diseases. The
CC antibodies are further used to treat a variety of other diseases or
CC conditions where it is desired to stimulate proliferation of
CC T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B
CC lymphocytes, to augment anti-infectious disease immunity, to induce CTL,
CC LAK or NK lytic activity, or to augment the destruction of tumour cells
CC or cells infected with virus. The present sequence represents a cDNA
XX encoding the simian ETF (SETF) polypeptide.

Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 22; Length 489;
Best Local Similarity 100.0%; Pred. No. 5,7e-117;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 ATGAGAAATTTGGAACCACTTTGAGAGATTTTCCATCCAGTCTACTTGTGTTACTT 60
Db 1 atgagaatttcgaacacacattgagaagtattccatccagtgctacttgttactt 60
Oy 61 CTAACAGATCTTTTCACTGAAGCTGGCATTCATGCTCTTCAATTTTGGCTGTTCACT 120
Db 61 ctataacagatcttctcaactgaagctggcatcatcattctcaatttggctgctcagt 120
Oy 121 GCAGGGCTTCCTAAACAGAGCAACTGGTGAATGTAATGATTTGAAAAAATTT 180
Db 121 gcagggcttccctaaacagagcaactggtgaaagtataagattgaaaaaat 180
Oy 181 GAAGATCTTATTCATCATCTATGCTATTTGCTACTTTATATAGGAAGATGATTTAC 240
Db 181 gaagatcttattcaatcatatgcatatgtacttatacgaagaagtatgttccac 240
Oy 241 CCCAGTTGCAAGTAACAGCAATGAAGTCTTCTTCTTGAGTTCAGTTTTCACCT 300
Db 241 cccagttgcaagtaacagcaatgaagtcttcttcttgagttacaagtatcttccact 300
Oy 301 GAGTCCGAGATGCAAGTATTTCATGATACATAGAAATCTGATGCTTACCAAAAC 360
Db 301 gagtccgagatgcaagtatttcgatgacatagaaaatctgatgaccttccaaacac 360
Oy 361 ACTTGTCTCTTAATGGGAATTCACAGAAATGTCAGAAAGATGTGAGCACTGGAG 420
Db 361 agttgtctctcaatgggaatgtacacagatctgagtcagaagtgtggaactgag 420
Oy 421 GAAAAAATATTAAAGAAATTTTTCAGAGTTTGTACATATTGTCCAAAGTTCATCAAC 480
Db 421 gaaaaaataataagaatttttgagaggtttgtacatatgtccaaatgtcatcac 480
Oy 481 ACTCTTGA 489
Db 481 actctctga 489

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RESULT 14
AA56368
ID AAX56368 standard; DNA: 1202 BP.

XX AAX56368;

XX 21-JUL-1999 (first entry)

XX Human IL-15 DNA.

XX Human: Interleukin 15; IL-15; ribozyme; enzymatic RNA; cleavage;

XX rheumatoid arthritis; inflammatory disorder; ds.

XX Homo sapiens.

XX WO9923208-A2.

XX 14-MAY-1999.

XX 29-OCT-1998; 98MO-IB01837.
 XX 31-OCT-1997; 97US-0962503.
 XX (HISM) HISAMITSU PHARM CO LTD.
 XX Hamanaka S, Nozawa I, Veerapaneni D;
 XX WPI, 1999-313334/26.
 XX
 XX New ribozymes targeted to interleukin-15 mRNA
 XX
 XX Disclosure: Fig 8; 46pp; English.
 XX
 XX The present sequence describes an isolated RNA molecule which
 XX specifically cleaves mRNA encoding interleukin 15 (IL-15). The
 XX enzymatic RNA molecules can bind to and cleave mRNA encoding IL-15.
 XX They can be used for treating disorders associated with IL-15 such
 XX as inflammatory disorders, e.g. rheumatoid arthritis by inhibiting
 XX the synthesis of IL-15 in lymphocytes and preventing the recruitment
 XX and activation of macrophages. They can also be used to develop
 XX transgenic animals which can be used to identify the impact of
 XX increased or decreased IL-15 levels on a particular pathway or
 XX phenotype. The present sequence represents a human IL-15 DNA sequence.
 XX
 XX Sequence 1202 BP; 355 A; 219 C; 249 G; 379 T; 0 other;

Query Match 100.0%; Score 489; DB 20; Length 1202;
 Best Local Similarity 100.0%; Pred. No. 7.2e-117;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 317 atgagatttcgaaccacattgagaagatttcacacagtgctacttgttactt 376
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 QY 61 CTAAAGATCTTTTCTTACTGAAAGTGGATTCATGCTCTTCTTGGCTGTTTCAGT 120
 |||||||
 DB 377 cttaaaagatcatttctactgaagctgacatcattcattcatttggcgttca 436
 |||||||
 QY 121 GCAGGCTTCCTAAACAGAGCCACTGGGTGATGTAATGATGATTTGAAAAAAT 180
 |||||||
 DB 437 gcaaggcttccttaaacagagcaactgggtgaagtaagtaagttgaaaaaat 496
 |||||||
 QY 181 GAAGATCTTATTCATCTGATGATTTGATGCTACTTTATATACGGAAGTGTTCAC 240
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 DB 497 gaagatcattcattcattcattcattcattcattcattcattcattcattc 556
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 QY 241 CCAGTTGCAAAAGTAAAGCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 300
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 DB 557 ccaagttgcaaaagtaagcaagtaagttgcttctcttggagtaagtaagtaag 616
 |||||||
 QY 301 GAGTCCGAGATGCAAGTATTCATGATACAGTAAATGATGATCCTAGCAAAAC 360
 |||||||
 DB 617 gactccgagatgcaagatcattcattcattcattcattcattcattcattcatt 676
 |||||||
 QY 361 AGTTTGTCTTCTAATGGGAATGTAACAGAAATGCGATGCAAAAGATGAGAG 420
 |||||||
 DB 677 agttgtcttctaattggaatgtaacagaaatcgtatgcaaaagatgtagaactgag 736
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 QY 421 GAAAAAATTTTAAAGATTTTGGAGATTTGACATTTGTCGCAAAATGTCATCAAC 480
 |||||||
 DB 737 gaaaaaataataagaatttcgcagagtttgtacataatgccaagttcattcaac 796
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 QY 481 ACTTCTTGA 489
 |||||||
 DB 797 acttcttga 805

RESULT 15
 AAF21342
 ID AAF21342 standard; DNA: 1202 BP.

XX AAF21342;
 AC 14-MAR-2001 (first entry)
 XX
 XX Human low adenosine antisense oligonucleotide related sequence #2909.
 DE
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiallergic; analgesic; hypotensive; cytosolic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200062736-A2.
 PN
 XX 26-OCT-2000.
 PD
 XX 24-MAR-2000; 2000MO-US08020.
 PF
 XX 06-APR-1999; 99US-0127958.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 XX NYCE JW:
 PI
 XX WPI, 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not
 XX trigger adenine receptors during metabolism, useful e.g. for treating
 XX cancers and respiratory obstructions -
 XX
 XX Disclosure: Page 1344-1345; 1592pp; English.
 XX
 XX The present invention describes low adenosine (A) content antisense
 XX oligonucleotides and compositions (I) comprising them. In the antisense
 XX oligonucleotides the A is replaced by a 'universal' or alternative base.
 XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 XX immunosuppressive, antiallergic, hypotensive and cytosolic activities.
 XX The antisense oligonucleotides and (I) can be used to down-regulate the
 XX expression and/or activity of target polypeptides associated with
 XX lung/respiratory disorders and malignancies, such as stimulating and
 XX activating peptide factors and transmitters, transcription factors,
 XX immunoglobulins and antibodies, antibody receptors, cytokines and
 XX chemokines, endogenously produced specific and non-specific enzymes,
 XX binding proteins, adhesion molecules and their receptors, cytokine and
 XX chemokine receptors, adenosine receptors, bradykinin receptors, central
 XX nervous system (CNS) and peripheral nervous and non-nervous system
 XX receptors, CNS and peripheral nervous and non-nervous system peptide
 XX transmitters, defensins, growth factors, vasoactive peptides and
 XX receptors, binding proteins and malignancy associated proteins. The
 XX antisense oligonucleotides may be used in this way to treat disorders
 XX including respiratory obstruction (especially pulmonary obstruction
 XX and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 XX and/or surfactant hypoproduction which are associated with a disease or
 XX condition selected from pulmonary vasoconstriction, inflammation,
 XX allergies, asthma, impeded respiration, respiratory distress syndrome
 XX (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 XX hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 XX pulmonary transplantation rejection, pulmonary infections, bronchitis,
 XX and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 XX fragments and antisense oligonucleotides used in the exemplification of
 XX the present invention.
 XX
 XX Sequence 1202 BP; 355 A; 219 C; 249 G; 379 T; 0 other;

Query Match	100.0%	Score 489;	DB 21;	Length 1202;
Best Local Similarity	100.0%;	Pred. No. 7.2e-117;		
Matches 489;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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OY	61	CTAAACACTCATTTTCTTAAGTGAAGCTGGCATTCATGTCTTCATTTTGGCTGTTCAAT	120
Db	377	ctaaacagtcacttctctaacggaagctggtcatcattgcttcaatttggcgtcttcagt	436
OY	121	GCAGGCGTTTCTTAAACGAAAGCCACTGGGTGANTGTAATTAAGTATTTGAAAAAATT	180
Db	437	gcagggtcttccaaagaagagccaaactgggtgaatgtaataagtgattgaaaaaat	496
OY	181	GAACATCTTATTCATCATGTATGATTTGATGATGCTTATATACGGAAATGATGTTTAC	240
Db	497	gaagatctctatccattctatgacatatgtgaigctactcttataacggaagtgctgtccag	556
OY	241	CCCACTTGCAAGTATACGACGATGAAGTGGTTTCTCTTGAGATTACAGTTATTTCACTT	300
Db	557	ccccagttgcagaagtaacagcaatgaagtgcttctctctgttgatcaagttattcactt	616
OY	301	GATGTCGGACATGCAAGCATTTCAATGATGATGAGTAAGTGAATAATGATTCATCCAGCAACAC	360
Db	617	gagtcgcggagatcgaaatattcatatgatacagtgaaaaatctgcatactccaaagaacac	676
OY	361	AGTTTGTCCTTCTAATGCGAATGTATACAGAACTCGATGCAAAAGAAATGTGAGAACTGGAG	420
Db	677	agtttgcttcttaatggaatgtacacgaatctcgatgcaagaatctgtagagaaactggag	736
OY	421	GAAAAAATATTTAAAGATTTTGGACAGTTTGTGCATATTTGTCCAAATGTTCAATCAC	480
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Db	797	acttcttga 805	

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2002, 23:04:52 ; Search time 2237.54 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	489	100.0	982	9	AL548180
2	430.2	88.0	994	9	AL572832
3	399.4	81.7	509	9	AA463370
4	348.8	71.3	800	10	BG184658
5	295.8	60.5	637	9	AI860008
6	292	59.7	756	10	BI832895
7	244	49.9	872	10	BI758686
8	210.6	43.1	826	10	BI685688
9	176.2	36.0	309	10	BF095213
10	174	35.6	471	10	N76741
11	166.6	34.1	690	9	AI596704
12	152.8	31.2	474	10	N49734
13	150.2	30.7	538	9	AI152482
14	150	30.3	515	10	BF704348
15	148.2	30.3	564	9	AA863763
16	139.6	28.5	631	9	BB661271
17	132.4	27.1	166	10	BF379349

18	116	23.7	181	9	AA497102
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20	106.2	21.7	590	9	AA544986
21	105.8	21.6	488	9	BB825167
22	103.2	21.1	430	9	AA858938
23	98.2	20.1	420	10	BE690327
24	90	18.4	550	10	BE698667
25	87.6	17.9	429	9	AA863979
26	86.2	17.6	648	9	AA874636
27	86	17.0	718	10	BI766231
28	83	17.0	434	9	AI503618
29	82	16.8	494	9	AA804168
30	75.6	15.5	405	9	AA121368
31	75.4	15.4	301	10	BF088290
32	74.4	15.2	509	9	AI120615
33	73.8	15.1	275	10	BF088272
34	72	14.7	483	9	AA804165
35	56	11.5	391	12	A2334843
36	55.8	11.4	278	9	BE177883
37	49.8	10.2	987	12	CNS014PQ
38	44	9.0	1101	12	CNS0039G
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40	43	8.8	1310	12	CNS0152W
41	42.4	8.7	1204	12	CNS016E2
42	42.2	8.6	1101	12	CNS000M2
43	42	8.6	1101	12	CNS017KX
44	41.2	8.4	1010	12	CNS07BNJ
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ALIGNMENTS

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DEFINITION prime, mRNA sequence.
ACCESSION AL548180
VERSION AL548180.1 GI:12882943
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 982)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1..982
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/db_xref="taxon:9606"
/clone="CS001034Y009"
/clone_lib="LTI_NFL006.PL2"
/tissue_type="placenta"
/note="Vector: PCWSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end was enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCWSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com 1 others
BASE COUNT 275 a 208 c 214 g 284 t
ORIGIN

Query Match 100.0%; Score 489; DB 9; Length 982;
 Best Local Similarity 100.0%; Pred. No. 1.8e-104; Mismatches 0; Indels 0; Gaps 0;
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 ACCESSION AL572832
 VERSION AL572832
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 994)
 AUTHORS Li, W. B., Gruber, C., Jesse, J., and Polyes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
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 /db_xref="taxon:9606"
 /clone="CS0D1034Y009"
 /clone_lib="LTI_NFL006_PL2"
 /issue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site: 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com
 BASE COUNT 333 a 186 c 154 g 316 t 5 others
 ORIGIN

Query Match 88.0%; Score 430 2; DB 9; Length 994;
 Best Local Similarity 98.6%; Pred. No. 1e-90; Mismatches 2; Indels 0; Gaps 0;
 Matches 429; Conservative 4;

55 TTACTTCTAAGATCTTATTCATCTATGATATGATGCTTCTTCACTTTTAAAGGAAAGTAT 114
 |||||||
 994 TTACTTCTAAGATCTTATTCATCTATGATATGATGCTTCTTCACTTTTAAAGGAAAGTAT 935
 |||||||
 115 TTCACTGAGGCTTCTTAAACAGAGCACTGGTGAATGTAATGATTTGAAAA 174
 |||||||
 934 TTCACTGAGGCTTCTTAAACAGAGCACTGGTGAATGTAATGATTTGAAAA 875
 |||||||
 175 AAAATGGAAGATCTTATTCATCTATGATATGATGCTTCTTCACTTTTAAAGGAAAGTAT 234
 |||||||
 874 AAAATGGAAGATCTTATTCATCTATGATATGATGCTTCTTCACTTTTAAAGGAAAGTAT 815
 |||||||
 235 GTTACCCCACTTTCGAAGTAAACAGCACTGATGCTTCTTCACTTTTAAAGGAAAGTAT 294
 |||||||
 814 GTTACCCCACTTTCGAAGTAAACAGCACTGATGCTTCTTCACTTTTAAAGGAAAGTAT 755
 |||||||
 295 TCACCTGAGTCCGAGATGCAAGTATTCATGATATGATGCTTCTTCACTTTTAAAGGAAAGTAT 354
 |||||||
 754 TCACCTGAGTCCGAGATGCAAGTATTCATGATATGATGCTTCTTCACTTTTAAAGGAAAGTAT 695
 |||||||
 355 AACAAAGTTTCTTCTTAAATGGAATGTAACAGAAATCTGATGCAAGAAATGTAAGAA 414
 |||||||
 694 AACAAAGTTTCTTCTTAAATGGAATGTAACAGAAATCTGATGCAAGAAATGTAAGAA 635
 |||||||
 415 CTGAGGAAAAAATATTTAAAGATTTTTCAGAGTTTTCATATTTGCAAAATGTTTTC 474
 |||||||
 634 CTGAGGAAAAAATATTTAAAGATTTTTCAGAGTTTTCATATTTGCAAAATGTTTTC 575
 |||||||
 475 ATCAACACTTCTTGA 489
 |||||||
 574 ATCAACACTTCTTGA 560

RESULT 3 AA463370 509 bp mRNA linear EST 10-JUN-1997
 LOCUS AA463370 2x97412.r1 Soares, Nihmpu, SI Homo sapiens cDNA clone IMAGE:811703 5,
 DEFINITION similar to SW:IL15_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ;, mRNA
 sequence.
 ACCESSION AA463370
 VERSION AA463370
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 509)
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Merra, M., Martin, J., Moore, B.,
 Schellenberg, K., Stepien, M., Tan, F., Theising, B., White, Y., Wyllie,
 T., Waterston, R., and Wilson, R.
 TITLE Washu-Merck EST Project 1997
 JOURNAL Unpublished (1997)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estelw@wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone; similarity on wrong strand. Seq primer: -28m13 rev2 ET from Amersham. High quality sequence stop: 416.

FEATURES

SOURCE

1. 509
/organism="Homo sapiens"
/db_xref="GDB:6042614"
/db_xref="taxon:9606"
/clone="IMAGE:811703"
/clone_1lb="Scarses_NbHMPu.S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site: 1: Not 1; Site: 2: Eco RI. Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDHM, pregnant uterus NBHPU, and fetal heart NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT
ORIGIN

149 a 91 c 108 g 161 t

Query Match 81.7%; Score 399.4; DB 9; Length 509;
Best Local Similarity 99.8%; Pred. No. 1.6e-83;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGGAATTCGAAACACATTTGAGAAGTATTCATCCAGTGCCTACTTGTCTTACTT 60
|||||
105 ATGGAATTCGAAACACATTTGAGAAGTATTCATCCAGTGCCTACTTGTCTTACTT 164
|||||
61 CTAAACAGTATTTCTTACTGAAAGTGCATTCATCTTCTTATTTGGCTGTTTCACT 120
|||||
165 CTAAACAGTATTTCTTACTGAAAGTGCATTCATCTTCTTATTTGGCTGTTTCACT 224
|||||
121 GCAGGCTTCTTAACAGAACCACTGGTGAATGAATGAATGAATGAATGAATGAAT 180
|||||
225 GCAGGCTTCTTAACAGAACCACTGGTGAATGAATGAATGAATGAATGAATGAAT 284
|||||
181 GAAGATCTTATTCATCTATGATGCTACTTATTAATAGGAAAGTATGATGTTTCA 240
|||||
285 GAAGATCTTATTCATCTATGATGCTACTTATTAATAGGAAAGTATGATGTTTCA 344
|||||
241 CCCAGTTCGAAAGTACAGCAATGAAGTCTTCTTGGAGTTACAAAGTATTTCACTT 300
|||||
345 CCCAGTTCGAAAGTACAGCAATGAAGTCTTCTTGGAGTTACAAAGTATTTCACTT 404
|||||
301 GAGTCCGAGATGCAAGTATTCATGATACAGTAAATTCGATCATCTAGCAAAACAC 360
|||||
405 GAGTCCGAGATGCAAGTATTCATGATACAGTAAATTCGATCATCTAGCAAAACAC 464
|||||
361 AGTTGCTCTTAATGGAGATGTAACAGAAATCTGCATCAA 401
|||||
465 AGTTGCTCTTAATGGAGATGTAACAGAAATCTGCATCAA 505
|||||

RESULT

LOCUS

BG184658 800 bp mRNA linear EST 21-APR-2001

DEFINITION

RS37320 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION

BG184658.1 GI:13706473

KEYWORDS

EST.

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 800)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J.,
Lerner, B., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,
E., Veloso, N., Klinka, A., Hess, J., Colthron, K., Lo, K., Offenbacher,
J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave. Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 444.

JOURNAL

MEDLINE

COMMENT

FEATURES

SOURCE

1. 800
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="Athersys RAGE Library"
/cell_line="H1080"
/note="See 'Creation of Genome-Wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."

BASE COUNT
ORIGIN

235 a 151 c 165 g 247 t

Query Match 71.3%; Score 348.8; DB 10; Length 800;
Best Local Similarity 90.4%; Pred. No. 1.2e-71;
Matches 441; Conservative 0; Mismatches 37; Indels 10; Gaps 6;

1 ATGGAATTCGAAACACATTTGAGAAGTATTCATCCAGTGCCTACTTGTCTTACTT 60
|||||
265 ATGGAATTCGAAACACATTTGAGAAGTATTCATCCAGTGCCTACTTGTCTTACTT 324
|||||
61 CTAAACAGTATTTCTTACTGAAAGTGCATTCATCTTCTTATTTGGCTGTTTCACT 120
|||||
325 CTAAACAGTATTTCTTACTGAAAGTGCATTCATCTTCTTATTTGGCTGTTTCACT 384
|||||
121 GCAGGCTTCTTAACAGAACCACTGGTGAATGAATGAATGAATGAATGAATGAAT 180
|||||
385 GCAGGCTTCTTAACAGAACCACTGGTGAATGAATGAATGAATGAATGAATGAAT 444
|||||
181 GAAGATCTTATTCATCTATGATGCTACTTATTAATAGGAAAGTATGATGTTTCA 240
|||||
445 GAAGATCTTATTCATCTATGATGCTACTTATTAATAGGAAAGTATGATGTTTCA 504
|||||
241 CCCAGTTCGAAAGTACAGCAATGAAGTCTTCTTGGAGTTACAAAGTATTTCACTT 300
|||||
505 CCCAGTTCGAAAGTACAGCAATGAAGTCTTCTTGGAGTTACAAAGTATTTCACTT 564
|||||
301 GAGTCCGAGATGCAAGTATTCATGATACAGTAAATTCGATCATCTAGCAAAACAC 360
|||||
565 GAGTCCGAGATGCAAGTATTCATGATACAGTAAATTCGATCATCTAGCAAAACAC 622
|||||
623 A-TTTGGCTTCTAATGGATGGT--ACAAATCTGGTGAAGATGGAAGACCTGAA 678
|||||
421 GAAAAAATTAATGAATTTTGGAGAGTTTGTACATATTTGCCAATGTCATCAAC 480
|||||
679 G--AAAAATTTAAGAAATTTTGAAGATTTTGGCTATTTGG--CCAATGTTCTCAAC 734
|||||
481 ACTCTTG 488
|||||
735 ACTTTTG 742
|||||

RESULT	5
LOCUS	A1860008/C
DEFINITION	A1860008 637 bp mRNA linear EST 07-MAR-2000 wM22g93.x1 NCI-CGAP ut4 Homo sapiens cDNA clone IMAGE:2436724 3'
ACCESSION	similar to SW:U115_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ;, mRNA sequence.
VERSION	A1860008
KEYWORDS	A1860008.1 GI:5513624
SOURCE	EST.
ORGANISM	human. Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 637)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, ph.D.

FEATURES	Location/Qualifiers
source	1. .637

BASE COUNT ORIGIN	207 a	111 c	91 g	227 t	1 others
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Query Match	60.5%	Score 295.8;	DB:9;	Length 637;
Best Local Similarity	99.0%	Pred No 30.50;		

Matches	297;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	----	--------	----	------	----

190 ATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGATGTTCAACCCAGTTGC 249

Db 637 ATTCATCTATGCATATTGATGCTACTTAATATATACGGAAGTGATGTTCACTCCAGTTGC 578

250 AAAGTACAGCAATGAAGTGTCTTCTCTTGAGTTACAACTTATTTCACCTTGAGTCCGGA 309

Db 577 AAAGTANCAGCAATGAAGTCCTTCTCTTGGAGTTACAAGTTATTTCACCTTGAGTCCGA 518

310 GATGCAAGTATTCATGATACAGTAGAAATCTGATCATCTAGCAACACACAGTTTGTCT 369

Db 517 GATGCAAGTATTCATGATACAGTAGAAATCTGATCATCTAGCAACACAGTTGTCT 458

370 TCTAATGGGAATGTACAGAATCTGGATGCCAAGAATCTGAGGAAGCTGGAGGAAAAAAT 429

Db 457 TCTAATGGGATGTACAGAATCTGGATGCCAAGAATGTGAGGAATCTGGAAGGAAAAAT 398

430 ATTAAGAATTTTGCAGAGTTTGTACATAATTGTCCTTCAATGTTTCATCAACACTTCTTCA 488

Db 397 ATTAAAGATTTTTCAGAGTTTGTACATATTGTCCTCAATGTTTCATCAACACCTCTCTCA 338

RESULT	6
LOCUS	BI832895
DEFINITION	BI832895 756 bp mRNA linear EST 04-OCT-2001
ACCESSION	60308247801 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:521771 5',
VERSION	BI832895.1 GI:15944445
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
TITLE	1 (bases 1 to 756)
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaps-remail.nih.gov

source 1. .756

BASE COUNT	247 a	115 c	143 g	251 t
ORIGIN				

Query Match	59.7%	Score 292;	DB 10;	Length 756;
Best local similarity	99.4%	Prod No. 3	40-50;	.

Matches	314;	Conservative	0;	Mismatches	0;	Indels	2;	Gaps	2;
---------	------	--------------	----	------------	----	--------	----	------	----

174 AAAAATTGAGATCTTATTCAATCTATGCATATTGATGCTACTTATATACGGAAGTGA 233

Db 1 AAAAATTGAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGA 60

234 TGTTCACCCCAGTTGCAAGTAACAGCAATGAAGTGCTTCTCTTGAGTTACAAGTTAT 293

Db 61 TGTTCACCCAGTTGCAAGTAACAGCAATGAAGTGCCTTCTCTTGAGTTACAAGTTAT 120

294 TTCACCTGAGTCCGAGATGCAAGTATTCATGATACAGTAGAATACTGATCATCCTAGC 353

Db 121 TTCACTTGAGTCCGAGATGCAAGTATTCATGATACAGTAGAATCTGATCATCCTAGC 180

354 AAACAACAGTTTGTCTTCTAATGGGAATGTAACAGAATCTGGATGCCAAAGAATGTGAGGA 413

Db 181 AACACACAG-TTGTCTTCTAATGGGAATGTACAGAACTGGATGCCAAGAATGTGAGGA 239

414 ACTGGAGGAAAAAATATTAAAGCAATTTTGCAGAGTTTGTACATATTGTCCAAATGTT 473

Db 240 ACTGAGGAAAAATATTAAAGAA TTTTGCAGAGTTTGTACATA-TGTCCAATGTT 298

OY 474 CATCACACTTCTTGA 489
|||||
Db 299 CATCACACTTCTTGA 314

RESULT 7
BI758686 872 bp mRNA linear EST 25-SEP-2001
LOCUS 603024240F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5194977 5',
DEFINITION mRNA sequence.
ACCESSION BI758686
VERSION BI758686.1 GI:15750264
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 872)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>,
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11877 row: 0 column: 10
High quality sequence start: 24
High quality sequence stop: 859.
Location/Qualifiers

FEATURES

source

1..872
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5194977"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is Oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
BASE COUNT 200 a 222 c 227 g 223 t
ORIGIN

Query Match 49.9%; Score 244; DB 10; Length 872;
Best Local Similarity 98.9%; Pred. No. 4.1e-47;
Matches 277; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

OY 1 ATGAGATTTCGAACACATTTGAGAAGATTTCCATCCAGTGTACTTGTTACTT 60
|||||
Db 592 ATGAGATTTCGAACACATTTGAGAAGATTTCCATCCAGTGTACTTGTTACTT 651
OY 61 CTAACAGTCATTTTCTAACTGAAGTGCATTCATGCTCTTCAATTTGGGCTGTTCACT 120
|||||
Db 652 CTAACAGTCATTTTCTAACTGAAGTGCATTCATGCTCTTCAATTTGGGCTGTTCACT 711
OY 121 GCAGGCTTCCTAAACAGACCACTGGGTGAATGTAATAGTATTTGA-AAAAAT 179
|||||
Db 712 GCAGGCTTCCTAAACAGACCACTGGGTGAATGTAATAGTATTTGA-AAAAAT 771
OY 180 TGAAGATCTTATTCATCTATGATATGATGCTACTTATATATAGGAAGTGATGTCA 239
|||||
Db 772 TGAAGATCTTATTCATCTATGATATGATGCTACTTATATATAGGAAGTGATGTCA 831

OY 240 -CCCCAGTTGCAAGTAACA-GCAATGAGTGCCTTCT 277
|||||
Db 832 CCCCCAGTTGCAAGTAACAAGTGAAGTGCCTTCT 871

RESULT 8
BI685688 826 bp mRNA linear EST 18-SEP-2001
LOCUS 603309529F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5345382 5',
DEFINITION mRNA sequence.
ACCESSION BI685688
VERSION BI685688.1 GI:15648316
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 826)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>,
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11877 row: j column: 07
High quality sequence stop: 826.
Location/Qualifiers

FEATURES

source

1..826
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5345382"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT 212 a 218 c 174 g 222 t
ORIGIN

Query Match 43.1%; Score 210.6; DB 10; Length 826;
Best Local Similarity 79.4%; Pred. No. 2.7e-39;
Matches 274; Conservative 0; Mismatches 69; Indels 2; Gaps 2;

OY 1 ATGAGATTTCGAACACATTTGAGAAGATTTCCATCCAGTGTACTTGTTACTT 60
|||||
Db 481 ATGAGATTTCGAACACATTTGAGAAGATTTCCATCCAGTGTACTTGTTACTT 540
OY 61 CTAACAGTCATTTTCTAACTGAAGTGCATTCATGCTCTTCAATTTGGGCTGTTCACT 120
|||||
Db 541 CTAACAGTCATTTTCTAACTGAAGTGCATTCATGCTCTTCAATTTGGGCTGTTCACT 599
OY 121 GCAGGCTTCCTAAACAGACCACTGGGTGAATGTAATAGTATTTGA-AAAAAT 180
|||||
Db 600 GTAGGCTTCCTAAACAGACCACTGGGTGAATGTAATAGTATTTGA-AAAAAT 659
OY 181 GAAGATCTTATTCATCTATGATATGATGCTACTTATATATAGGAAGTGATGTCA 240
|||||
Db 660 GAAGATCTTATTCATCTATGATATGATGCTACTTATATATAGGAAGTGATGTCA 718
OY 241 CCCAGTTGCAAGTAACAAGTGAAGTGCCTTCTTGTGAGTTCACAACTTATTTCACTT 300
|||||

Db 719 CCCAGTTCGAAGATTACTGCAATGACGCTTTCCTCGAATTGCCGGTTATTATTTACAT 778
 Oy 301 GAGTCCGGAGATGCAAGTATTTCATGATCAGTACGAATAATTCGATC 345
 Db 779 GAGTACAGTAACATGACTCTTAATGAAACAGTAAAGAACGTGCTC 823

RESULT 9
 BF095213 309 bp mRNA linear EST 19-OCT-2000
 LOCUS IL2-UT0071-050900-144-B03 UT0071 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF095213
 VERSION BF095213.1 GI:10900923
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 309)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunslein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=et2-IL2-UT0071-050
 900-144-B03&t3=2000-09-05&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 309.
 Location/Qualifiers
 1..309
 /organism="Homo sapiens"
 /db_xref="taxon:3606"
 /clone_lib="UT0071"
 /dev_stage="Adult"
 /note="Organ: uterus; tumor; Vector: puc18; Site_1: Sma1;
 Site_2: Sma1; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 Profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 110 a 48 c 55 g 96 t
 ORIGIN

Query Match 36.0%; Score 176.2; DB 10; Length 309;
 Best Local Similarity 98.3%; Pred. No. 2.9e-31;
 Matches 178; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 309 AGATCAAGTATTCATGATACGTAGAAATCTGATCATCTCAAGCAACAGTTTCTC 368
 Db 1 AGATCAAGTATTCATGATACGTAGAAATCTGATCATCTCAAGCAACAGTTTCTC 60
 Oy 369 TTCATATGGATGTAACAGATTCGATGCAAGAAATGAGGAAGTGGAGAAAAA 428
 Db 61 TTCTATATGGATGTAATAGATTCGATGCAAGAAATGAGGAAGTGGAGAAAAA 120
 Oy 429 TATTAAAGATTTCGACAGCTTTTGTACATATGTGCCAATGTTTCATCAACACTTCTTG 488

Db 121 TATTAAAGATTTCGACAGATTTCATATATTCGCCAATGTTTCATCAACACTTCTTG 180
 Oy 489 A 489
 Db 181 A 181

RESULT 10
 N76741 471 bp mRNA linear EST 02-APR-1996
 LOCUS N76741
 DEFINITION yz82g12.1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA
 clone IMAGE:289606 5' similar to SW:IL15_HUMAN P40933
 INTERLEUKIN-15 PRECURSOR ; mRNA sequence.
 N76741
 VERSION N76741.1 GI:1239319
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 471)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
 M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
 Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
 R., Williamson,A., Wohlmann,P. and Wilson,R.
 The Washu-Merck EST Project
 Unpublished (1995)
 JOURNAL MEDLINE
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: reverse ET
 High quality sequence stop: 296.
 Location/Qualifiers
 1..471
 /organism="Homo sapiens"
 /db_xref="GDB:3905446"
 /db_xref="taxon:3606"
 /clone="IMAGE:289606"
 /clone_lib="Soares_multiple_sclerosis_2NBHMSF"
 /sex="male"
 /tissue_type="multiple sclerosis lesions"
 /dev_stage="Age 46"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Vector: pRT3D (Pharmacia) with a modified
 polylinker V-type; phagemid; Site_1: Not I; Site_2: Eco RI
 primer 15',
 TGTTCACATCTGAAGTGGAGCGGCCCATTTTCTTTTCTTTT 3',
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pRT3D vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis
 lesions from one patient was kindly provided by Dr. Kevin
 G. Becker (NINDS/NIH)."
 BASE COUNT 161 a 68 c 83 g 154 t 5 others
 ORIGIN

Query Match 35.6%; Score 174; DB 10; Length 471;
 Best Local Similarity 97.4%; Pred. No. 9.8e-31;
 Matches 185; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Db 301 GAGTCCGGAGATGCAAGTATTCATGATACGTAAGAAATCTGATCATCTCAAGCAAC 360
 Db 4 GAGTCCGGAGATGCAAGTATTCATGATACGTAAGAAATCTGATCATCTCAAGCAAC 63

QY 361 AGTTGCTCTTAATGGAGATGTAACAGATCTGGATGCAAGAATGAGGAACCTGGAG 420
 Db 64 AGTTGCTCTTAATGGAGATGTAACAGATCTGGATGCAAGAATGAGGAACCTGGAG 123
 QY 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGCCAAATGTCAT-CAA 479
 Db 124 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGCCAAATGTCAT-CAA 183
 QY 480 CACTTCTTGA 489
 Db 184 CACTTCTTGA 193
 RESULT 11
 A1596704
 LOCUS 690 bp mRNA linear EST 21-APR-1999
 DEFINITION V38h11.y1 Soares_mammary_gland_NBMNG Mus musculus cDNA clone
 IMAGE:948933 5' similar to gb:U14332 Mus musculus interleukin 15
 (MOUSE); mRNA sequence.
 A1596704
 ACCESSION A1596704.1 GI:4605752
 VERSION EST.
 KEYWORDS house mouse.
 SOURCE Mus musculus.
 ORGANISM Mus musculus.
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 690)
 NCICGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:345789
 This read is a RESSEQUENCE of a previously sequenced mouse clone
 This read has been verified (found to hit its original self in the
 correct orientation)
 Seq primer: -40RP from G1bco
 High quality sequence stop: 466.
 Location/Qualifiers
 1. 690
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:948933"
 /clone_lib="Soares_mammary_gland_NBMNG"
 /sex="male"
 /tissue_type="mammary gland"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /note="Organ: mammary gland; Vector: p773D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
 RI; 1st strand cDNA was primed with a Not I - oligo(dT)
 primer [5'
 TGTACCAATCTGAAGTGGAGCGCGCGCAATGTTTTTTTTTTTTTTTTTTTTTTT
 T 3'] double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified p773 vector.
 RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
 constructed and normalized by Bento Soares and M. Fatima
 Bonaldo."

BASE COUNT 178 a 177 c 158 g 170 t 7 others
 ORIGIN

Query Match 34.1%; Score 166.6; DB 9; Length 690;
 Best Local Similarity 81.5%; Pred. No. 5.4e-29;
 Matches 190; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACATTGAGAGATTTCATCCAGTCGCTACTGTTGTTACTT 60

Db 450 ATGAAATTTTGAACCTATATATGAGATACATCCATCTGCTACTGTTCTT 509
 QY 61 CTAACAGTCATTTTCTAAGTGAAGCTGCATTCATGCTTCTTTGGCTGTTTCACT 120
 Db 510 CTAACAGTCATTTTCTAAGTGAAGCTGCATTCATGCTTCTTTGGCTGTTTCACT 569
 QY 121 GCAGGCTCTCTTAACAGAGCCCACTGGGTGAATGATATAGTATTTGAAAAAATT 180
 Db 570 GTAGCTCTCCCTAAACAGAGCCCACTGGGTGAATGATATAGTATTTGAAAAAATT 629
 QY 181 GAAGATCTTATTCATATGATATGATGCTCTTATATAGCAAGTGA 233
 Db 630 GAAGATCTTATTCATATGATATGATGCTCTTATATAGCAAGTGA 682

RESULT 12
 N49734/c
 LOCUS 474 bp mRNA linear EST 14-FEB-1996
 DEFINITION y206b12.s1 Soares_multiple_sclerosis_2NBHNSP Homo sapiens cDNA
 clone IMAGE:282239 3' similar to SW:1115_HUMAN P40933
 INTERLEUKIN-15 PRECURSOR; mRNA sequence.
 N49734
 ACCESSION N49734.1 GI:1190900
 VERSION EST.
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens.
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 474)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston
 R., Williamson, A., Wohlmann, P., and Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 Contact: Wilison RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: m13 -40 forward
 High quality sequence stop: 263.
 Location/Qualifiers
 1. 474
 /organism="Homo sapiens"
 /db_xref="GDB:3900767"
 /db_xref="taxon:9606"
 /clone="IMAGE:282239"
 /clone_lib="Soares_multiple_sclerosis_2NBHNSP"
 /sex="male"
 /tissue_type="multiple sclerosis lesions"
 /dev_stage="Age 46"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Vector: p773D (Pharmacia) with a modified
 polylinker V-type; phagemid; Site_1: Not I; Site_2: Eco RI
 ; 1st strand cDNA was primed with a Not I - oligo(dT)
 primer [5'
 TGTACCAATCTGAAGTGGAGCGCGCGCAATGTTTTTTTTTTTTTTTTTTTTTTT
 T 3'] double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified p773 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot - 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis
 lesions from one patient was kindly provided by Dr. Kevin
 G. Becker (NINDS/NIH).

FEATURES

source

BASE COUNT

160 a 81 c 67 g 161 t 5 others

ORIGIN

Search completed: June 19, 2002, 00:50:34
Job time: 6342 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 01:32:22 ; Search time 2151.24 Seconds
(without alignments)
4756.827 Million cell updates/sec

Title: US-09-724-841-4
Perfect score: 489
Sequence: 1 ATGAGATTTCGAAACCA.....TGTTCATCAACACTTCTGA 489

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	489	100.0	489	6	AR004267	AR004267 Sequence
2	489	100.0	489	6	AR024348	AR024348 Sequence
3	489	100.0	489	6	AR070282	AR070282 Sequence
4	489	100.0	489	6	AR085741	AR085741 Sequence
5	489	100.0	489	6	AR122045	AR122045 Sequence
6	489	100.0	489	6	AR122867	AR122867 Sequence
7	489	100.0	489	6	AR125104	AR125104 Sequence
8	489	100.0	489	6	AX006785	AX006785 Sequence
9	489	100.0	489	6	125782	125782 Sequence
10	489	100.0	489	6	128850	128850 Sequence
11	489	100.0	489	6	179220	179220 Sequence
12	489	100.0	1275	9	CAU03099	003099 Cercopithec
13	484.2	99.0	492	9	AB000555	AB000555 Macaca fa
14	484.2	99.0	559	6	MMU19843	U19843 Macaca mula
15	465	95.1	489	6	AR004268	AR004268 Sequence
16	465	95.1	489	6	AR024349	AR024349 Sequence
17	465	95.1	489	6	AR070281	AR070281 Sequence
18	465	95.1	489	6	AR085740	AR085740 Sequence
19	465	95.1	489	6	AR122046	AR122046 Sequence
20	465	95.1	489	6	AR122868	AR122868 Sequence
21	465	95.1	489	6	AR125105	AR125105 Sequence
22	465	95.1	489	6	AX006786	AX006786 Sequence
23	465	95.1	489	6	AX320244	AX320244 Sequence
24	465	95.1	489	6	125783	125783 Sequence
25	465	95.1	489	6	128849	128849 Sequence
26	465	95.1	489	6	162692	162692 Sequence
27	465	95.1	489	6	179219	179219 Sequence
28	465	95.1	1202	6	AR103280	AR103280 Sequence
29	465	95.1	1202	6	AX024715	AX024715 Sequence
30	465	95.1	1202	6	AX301227	AX301227 Sequence
31	465	95.1	1202	6	HS014407	U14407 Human Inter
32	463.4	94.8	489	6	AR094649	AR094649 Sequence
33	463.4	94.8	489	6	BD008811	BD008811 Antagonis
34	458.6	93.8	489	6	AX320242	AX320242 Sequence
35	457	93.5	489	6	AR094650	AR094650 Sequence
36	457	93.5	489	6	BD008812	BD008812 Antagonis
37	430.6	88.1	489	6	HS115MR	238000 H.sapiens m
38	385	78.7	489	4	BTU02433	U02433 Bos taurus
39	381.8	78.1	489	4	SSU58142	U58142 Sus scrofa
40	375.4	76.8	489	4	AF149700	AF149700 Ovis arlie
41	372.2	76.1	489	4	AF108148	AF108148 Felis cat
42	359.2	73.5	643	9	HS115MR1	X94222 H.sapiens m
43	359.2	73.5	643	9	HS115MR2	X94223 H.sapiens m
44	357.6	73.1	1248	6	AR087004	AR087004 Sequence
45	357.6	73.1	1248	9	AF031167	AF031167 Homo sap1

ALIGNMENTS

RESULT 1	489 bp	DNA	linear	PAT 04-DEC-1998
LOCUS AR004267				
DEFINITION Sequence 1 from patent US 5747024.				
ACCESSION AR004267				
VERSION AR004267.1	GI:3965146			
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 489)			
AUTHORS	Grabstein,K.H. and Widmer,M.B.			
TITLE	Vaccine adjuvant comprising Interleukin-15			
JOURNAL	Patent: US 5747024-A 1 05-MAY-1998;			
FEATURES	Location/Qualifiers			
source	1..489			
BASE COUNT	162 a 81 c 92 g 154 t			
ORIGIN				
Query Match	100.0%;	Score 489;	DB 6;	Length 489;
Best Local Similarity	100.0%;	Pred. No. 5,4e-91;		

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTCGAAACACATTTGAGAGTATTCATCCAGTGTACCTGTGTTACTT 60
|
Db 1 ATGGAATTCGAAACACATTTGAGAGTATTCATCCAGTGTACCTGTGTTACTT 60
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QY 61 CTAAGAGTCATTTTCTAAGTGAAGCGATTCATGCTTCTTATTTGGGCTGTTCAGT 120
|
Db 61 CTAAGAGTCATTTTCTAAGTGAAGCGATTCATGCTTCTTATTTGGGCTGTTCAGT 120
|
QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAAATGTAATGATTTGAAAAAATT 180
|
Db 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAAATGTAATGATTTGAAAAAATT 180
|
QY 181 GAAGATCTTATTCATATGATGATTTGATGCTTCTTATTCAGAAAGTATGTTTAC 240
|
Db 181 GAAGATCTTATTCATATGATGATTTGATGCTTCTTATTCAGAAAGTATGTTTAC 240
|
QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGAGTTGCAAGTTATTTACAT 300
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Db 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGAGTTGCAAGTTATTTACAT 300
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QY 301 GAGTCCGGAGATACAGATATTCATGATAGTAAATCTTATCTCTAGCAAAACAC 360
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Db 301 GAGTCCGGAGATACAGATATTCATGATAGTAAATCTTATCTCTAGCAAAACAC 360
|
QY 361 ATCTTGTCTTCTAATGGAATATACAGATCTGATGCAAGAAATGTGAGAACTAGAG 420
|
Db 361 ATCTTGTCTTCTAATGGAATATACAGATCTGATGCAAGAAATGTGAGAACTAGAG 420
|
QY 421 GAAAAAATATTAAAGATTTTTCGAGATTTTGTACATATTTGCCAAATGTTCAATCAAC 480
|
Db 421 GAAAAAATATTAAAGATTTTTCGAGATTTTGTACATATTTGCCAAATGTTCAATCAAC 480
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QY 481 ACTTCTTGA 489
|
Db 481 ACTTCTTGA 489
|

RESULT 2

AR024348 489 bp DNA linear PAT 05-DEC-1998

LOCUS AR024348
DEFINITION Sequence 1 from patent US 5795966.
ACCESSION AR024348
VERSION AR024348.1 GI:3977642
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.T.
TITLE Antagonists of interleukin-15
JOURNAL Patent: US 5795966-A 1 18-AUG-1998;
FEATURES
source 1. 489
location/Qualifiers

BASE COUNT 162 a 81 c 92 g 154 t

ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 5.4e-91;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTCGAAACACATTTGAGAGTATTCATCCAGTGTACCTGTGTTACTT 60
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Db 1 ATGGAATTCGAAACACATTTGAGAGTATTCATCCAGTGTACCTGTGTTACTT 60
|
QY 61 CTAAGAGTCATTTTCTAAGTGAAGCGATTCATGCTTCTTATTTGGGCTGTTCAGT 120
|
Db 61 CTAAGAGTCATTTTCTAAGTGAAGCGATTCATGCTTCTTATTTGGGCTGTTCAGT 120
|
QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAAATGTAATGATTTGAAAAAATT 180
|
Db 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAAATGTAATGATTTGAAAAAATT 180
|
QY 181 GAAGATCTTATTCATATGATGATTTGATGCTTCTTATTCAGAAAGTATGTTTAC 240
|
Db 181 GAAGATCTTATTCATATGATGATTTGATGCTTCTTATTCAGAAAGTATGTTTAC 240
|
QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGAGTTGCAAGTTATTTACAT 300
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Db 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGAGTTGCAAGTTATTTACAT 300
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QY 301 GAGTCCGGAGATACAGATATTCATGATAGTAAATCTTATCTCTAGCAAAACAC 360
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QY 361 ATCTTGTCTTCTAATGGAATATACAGATCTGATGCAAGAAATGTGAGAACTAGAG 420
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Db 361 ATCTTGTCTTCTAATGGAATATACAGATCTGATGCAAGAAATGTGAGAACTAGAG 420
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QY 421 GAAAAAATATTAAAGATTTTTCGAGATTTTGTACATATTTGCCAAATGTTCAATCAAC 480
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Db 481 ACTTCTTGA 489
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Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTCGAAACACATTTGAGAGTATTCATCCAGTGTACCTGTGTTACTT 60
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Db 1 ATGGAATTCGAAACACATTTGAGAGTATTCATCCAGTGTACCTGTGTTACTT 60
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QY 61 CTAAGAGTCATTTTCTAAGTGAAGCGATTCATGCTTCTTATTTGGGCTGTTCAGT 120
|
Db 61 CTAAGAGTCATTTTCTAAGTGAAGCGATTCATGCTTCTTATTTGGGCTGTTCAGT 120
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QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAAATGTAATGATTTGAAAAAATT 180
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Db 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAAATGTAATGATTTGAAAAAATT 180
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QY 181 GAAGATCTTATTCATATGATGATTTGATGCTTCTTATTCAGAAAGTATGTTTAC 240
|
Db 181 GAAGATCTTATTCATATGATGATTTGATGCTTCTTATTCAGAAAGTATGTTTAC 240
|
QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGAGTTGCAAGTTATTTACAT 300
|
Db 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGAGTTGCAAGTTATTTACAT 300
|

RESULT 3

AR070282 489 bp DNA linear PAT 18-FEB-2000

LOCUS AR070282
DEFINITION Sequence 4 from patent US 5892001.
ACCESSION AR070282
VERSION AR070282.1 GI:7221170
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Epstein-Barr virus-derived T-cell factor antibodies
JOURNAL Patent: US 5892001-A 4 06-APR-1999;
FEATURES
source 1. 489
location/Qualifiers

BASE COUNT 162 a 81 c 92 g 154 t

ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 5.4e-91;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTCGAAACACATTTGAGAGTATTCATCCAGTGTACCTGTGTTACTT 60
|
Db 1 ATGGAATTCGAAACACATTTGAGAGTATTCATCCAGTGTACCTGTGTTACTT 60
|
QY 61 CTAAGAGTCATTTTCTAAGTGAAGCGATTCATGCTTCTTATTTGGGCTGTTCAGT 120
|
Db 61 CTAAGAGTCATTTTCTAAGTGAAGCGATTCATGCTTCTTATTTGGGCTGTTCAGT 120
|
QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAAATGTAATGATTTGAAAAAATT 180
|
Db 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAAATGTAATGATTTGAAAAAATT 180
|
QY 181 GAAGATCTTATTCATATGATGATTTGATGCTTCTTATTCAGAAAGTATGTTTAC 240
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Db 181 GAAGATCTTATTCATATGATGATTTGATGCTTCTTATTCAGAAAGTATGTTTAC 240
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QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGAGTTGCAAGTTATTTACAT 300
|
Db 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGAGTTGCAAGTTATTTACAT 300
|

QY 301 GAGTCCGAGATACAGATATTCATGATACAGTACAGAAATCTTATCATCTCTAGCAAAACAC 360
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Db 301 GAGTCCGAGATACAGATATTCATGATACAGTACAGAAATCTTATCATCTCTAGCAAAACAC 360
QY 361 ATCTGTCTCTTAATGGAATATATACAGATCTGATCAAAAGATGAGAACTAGAG 420
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Db 361 ATCTGTCTCTTAATGGAATATATACAGATCTGATCAAAAGATGAGAACTAGAG 420
QY 421 GAAAAAATATTAAGAAATTTTTCAGAGATTTGTACATATTTGTCACAAATGTTTCACAC 480
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Db 421 GAAAAAATATTAAGAAATTTTTCAGAGATTTGTACATATTTGTCACAAATGTTTCACAC 480
QY 481 ACTTCTTGA 489
|||||
Db 481 ACTTCTTGA 489
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RESULT 4
AR085741 AR085741 489 bp DNA linear PAT 07-SEP-2000
LOCUS Sequence 4 from patent US 5985262.
DEFINITION AR085741
ACCESSION AR085741
VERSION AR085741.1 GI:10012507
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Method of treatment with epithelium derived T-cell factor
JOURNAL Patent: US 5985262-A 4 16-NOV-1999;
FEATURES
source 1..489
/organism="unknown"
BASE COUNT 162 a 81 c 92 g 154 t
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 5,4e-91;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTCGAACACATTTGAGAGATTTCCATCCAGTGCATCTGTCTTACTT 60
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Db 1 ATGAGATTTTCGAACACATTTGAGAGATTTCCATCCAGTGCATCTGTCTTACTT 60
QY 61 CTAAGAGTCAATTTTCTAATCTGAGTGGCATTCATGCTTCATTTTGGCTGTTTCA 120
|||||
Db 61 CTAAGAGTCAATTTTCTAATCTGAGTGGCATTCATGCTTCATTTTGGCTGTTTCA 120
QY 121 GCAGGCTCCCTAAACAGAGCAACTGGGTGAATTAAGTGAATTTGAAAAAAT 180
|||||
Db 121 GCAGGCTCCCTAAACAGAGCAACTGGGTGAATTAAGTGAATTTGAAAAAAT 180
QY 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 240
|||||
Db 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 ATCTGTCTCTTAATGGAATATATACAGATCTGATCAAAAGATGAGAACTAGAG 420
|||||
Db 241 ATCTGTCTCTTAATGGAATATATACAGATCTGATCAAAAGATGAGAACTAGAG 420
QY 301 GAGTCCGAGATACAGATATTCATGATACAGTACAGAAATCTTATCATCTCTAGCAAAAC 360
|||||
Db 301 GAGTCCGAGATACAGATATTCATGATACAGTACAGAAATCTTATCATCTCTAGCAAAAC 360
QY 361 ATCTGTCTCTTAATGGAATATATACAGATCTGATCAAAAGATGAGAACTAGAG 420
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Db 361 ATCTGTCTCTTAATGGAATATATACAGATCTGATCAAAAGATGAGAACTAGAG 420
QY 421 GAAAAAATATTAAGAAATTTTTCAGAGATTTGTACATATTTGTCACAAATGTTTCACAC 480
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Db 421 GAAAAAATATTAAGAAATTTTTCAGAGATTTGTACATATTTGTCACAAATGTTTCACAC 480

QY 481 ACTTCTTGA 489
|||||
Db 481 ACTTCTTGA 489
|||||
RESULT 5
AR122045 AR122045 489 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 1 from patent US 6165466.
DEFINITION AR122045
ACCESSION AR122045
VERSION AR122045.1 GI:14106362
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.
TITLE Antagonists of Interleukin-15
JOURNAL Patent: US 6165466-A 1 26-DEC-2000;
FEATURES
source 1..489
/organism="unknown"
BASE COUNT 162 a 81 c 92 g 154 t
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 5,4e-91;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTCGAACACATTTGAGAGATTTCCATCCAGTGCATCTGTCTTACTT 60
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Db 1 ATGAGATTTTCGAACACATTTGAGAGATTTCCATCCAGTGCATCTGTCTTACTT 60
QY 61 CTAAGAGTCAATTTTCTAATCTGAGTGGCATTCATGCTTCATTTTGGCTGTTTCA 120
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Db 61 CTAAGAGTCAATTTTCTAATCTGAGTGGCATTCATGCTTCATTTTGGCTGTTTCA 120
QY 121 GCAGGCTCCCTAAACAGAGCAACTGGGTGAATTAAGTGAATTTGAAAAAAT 180
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Db 121 GCAGGCTCCCTAAACAGAGCAACTGGGTGAATTAAGTGAATTTGAAAAAAT 180
QY 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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Db 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 CCAGTTGCAAGTACAGCAATGAAGTCTTCTCTGAGTGGCAAGTATTTTCAAT 300
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Db 241 CCAGTTGCAAGTACAGCAATGAAGTCTTCTCTGAGTGGCAAGTATTTTCAAT 300
QY 301 GAGTCCGAGATACAGATATTCATGATACAGTACAGAAATCTTATCATCTCTAGCAAAAC 360
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Db 301 GAGTCCGAGATACAGATATTCATGATACAGTACAGAAATCTTATCATCTCTAGCAAAAC 360
QY 361 ATCTGTCTCTTAATGGAATATATACAGATCTGATCAAAAGATGAGAACTAGAG 420
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Db 361 ATCTGTCTCTTAATGGAATATATACAGATCTGATCAAAAGATGAGAACTAGAG 420
QY 421 GAAAAAATATTAAGAAATTTTTCAGAGATTTGTACATATTTGTCACAAATGTTTCACAC 480
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Db 421 GAAAAAATATTAAGAAATTTTTCAGAGATTTGTACATATTTGTCACAAATGTTTCACAC 480
QY 481 ACTTCTTGA 489
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RESULT 6
AR122867 AR122867 489 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 1 from patent US 6168783.
ACCESSION AR122867

VERSION AR122867.1 GI:14107893
 KEYWORDS UNKNOWN.
 SOURCE UNKNOWN.
 ORGANISM UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 489)
 AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.
 TITLE Antagonists of Interleukin-15
 JOURNAL Patent: US 6168783-A 1 02-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..489
 BASE COUNT 162 a 81 c 92 g 154 t
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
 Best Local Similarity 100.0%; Pred. No. 5.4e-91;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGAGATTTCGAAACACATTTGAGAGATTTCATCCAGTGCCTGCTTACTT 60
 DB 1 ATGAGATTTCGAAACACATTTGAGAGATTTCATCCAGTGCCTGCTTACTT 60
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 DB 61 CTAAAGATCATTTTCTAATCTGAAAGCTGCATTGCTCTTCAATTTGGCGTTTCAGT 120
 OY 121 GCAGGGCTCCCTTAAACAGACCAAGCTGGTGAATGTAAAGATTGAAAAAATT 180
 DB 121 GCAGGGCTCCCTTAAACAGACCAAGCTGGTGAATGTAAAGATTGAAAAAATT 180
 OY 181 GAAGATCTTATTCATCTATGATATTTGATCTACTTTATATACAGAAAGTATGTCAC 240
 DB 181 GAAGATCTTATTCATCTATGATATTTGATCTACTTTATATACAGAAAGTATGTCAC 240
 OY 241 CCCAGTTGCAAGGTAAAGCAATGAAGTCTTCTCTTGGAGTGCAGATTATTTACAT 300
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 OY 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATGCTCTGCAAAACAC 360
 DB 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATGCTCTGCAAAACAC 360
 OY 361 ATCTTGCTTCTAATGGAATATTAACAGAAATCTGATGCAAAAGATGTGAGAACTAGAG 420
 DB 361 ATCTTGCTTCTAATGGAATATTAACAGAAATCTGATGCAAAAGATGTGAGAACTAGAG 420
 OY 421 GAAAAAATATTAAGAATTTTGGAGATTGTGACATATTGTCCTCAAAATGTTATCAAC 480
 DB 421 GAAAAAATATTAAGAATTTTGGAGATTGTGACATATTGTCCTCAAAATGTTATCAAC 480
 OY 481 ACTTCTTGA 489
 DB 481 ACTTCTTGA 489

RESULT 7
 LOCUS AR125104 489 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 1 from patent US 6177079.
 ACCESSION AR125104
 VERSION AR125104.1 GI:14111166
 KEYWORDS
 SOURCE UNKNOWN.
 ORGANISM UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 489)
 AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.
 TITLE Antagonists of Interleukin-15
 JOURNAL Patent: US 6177079-A 1 23-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..489

BASE COUNT 162 a 81 c 92 g 154 t
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
 Best Local Similarity 100.0%; Pred. No. 5.4e-91;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGAGATTTCGAAACACATTTGAGAGATTTCATCCAGTGCCTGCTTACTT 60
 DB 1 ATGAGATTTCGAAACACATTTGAGAGATTTCATCCAGTGCCTGCTTACTT 60
 OY 61 CTAAAGATCATTTTCTAATCTGAAAGCTGCATTGCTCTTCAATTTGGCGTTTCAGT 120
 DB 61 CTAAAGATCATTTTCTAATCTGAAAGCTGCATTGCTCTTCAATTTGGCGTTTCAGT 120
 OY 121 GCAGGGCTCCCTTAAACAGACCAAGCTGGTGAATGTAAAGATTGAAAAAATT 180
 DB 121 GCAGGGCTCCCTTAAACAGACCAAGCTGGTGAATGTAAAGATTGAAAAAATT 180
 OY 181 GAAGATCTTATTCATCTATGATATTTGATCTACTTTATATACAGAAAGTATGTCAC 240
 DB 181 GAAGATCTTATTCATCTATGATATTTGATCTACTTTATATACAGAAAGTATGTCAC 240
 OY 241 CCCAGTTGCAAGGTAAAGCAATGAAGTCTTCTCTTGGAGTGCAGATTATTTACAT 300
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 DB 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATGCTCTGCAAAACAC 360
 OY 361 ATCTTGCTTCTAATGGAATATTAACAGAAATCTGATGCAAAAGATGTGAGAACTAGAG 420
 DB 361 ATCTTGCTTCTAATGGAATATTAACAGAAATCTGATGCAAAAGATGTGAGAACTAGAG 420
 OY 421 GAAAAAATATTAAGAATTTTGGAGATTGTGACATATTGTCCTCAAAATGTTATCAAC 480
 DB 421 GAAAAAATATTAAGAATTTTGGAGATTGTGACATATTGTCCTCAAAATGTTATCAAC 480
 OY 481 ACTTCTTGA 489
 DB 481 ACTTCTTGA 489

RESULT 8
 LOCUS AX006785 489 bp DNA linear PAT 06-SEP-2000
 DEFINITION Sequence 3 from Patent WO0002582.
 ACCESSION AX006785
 VERSION AX006785.1 GI:9994821
 KEYWORDS
 SOURCE UNIDENTIFIED.
 ORGANISM UNIDENTIFIED.
 REFERENCE 1 (bases 1 to 489)
 AUTHORS Londel,M., Quarantino,S. and Maiuri,L.
 TITLE Treatment of coliac disease with interleukin-15 antagonists
 JOURNAL Patent: WO 0002582-A 3 20-JAN-2000;
 LONDEI MARCO (GB); QUARANTINO SONIA (GB); MATHILDA AND TERENCE KENNEDY I (GB); MAIURI LUIGI (IT)
 FEATURES Location/Qualifiers
 source 1..489
 BASE COUNT 162 a 81 c 92 g 154 t
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
 Best Local Similarity 100.0%; Pred. No. 5.4e-91;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAAATTTGAAACCCACATTTGGAGATTTTCCATCCAGCTGGTACTGGTTACTT	60
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QY	61	CTAAAGACTCATTTTCTAAGTGAAGCTGGCATTCATGCTTCAATTTTGGGCTGTTCA	120
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QY	121	GCAGGGGCTCCCTAAACAGAAAGCCAACTGGGATGTATTAAGCATTTGAAAAAATT	180
Db	121	GCAGGGGCTCCCTAAACAGAAAGCCAACTGGGATGTATTAAGCATTTGAAAAAATT	180
QY	181	GAAGATCTTATTCATCTATGCATATTGATGCTACTTATATACAGAAAGTATGTTAC	240
Db	181	GAAGATCTTATTCATCTATGCATATTGATGCTACTTATATACAGAAAGTATGTTAC	240
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Db	241	CCCAATTCCAGGTATACAGCAATGAAGCTTCTCTTGGAGTTGCAGTTATTTCA	300
QY	301	GAGTCCGAGATACAGATATTCATATACAGTATGATATGATATGATATGATATGAT	360
Db	301	GAGTCCGAGATACAGATATTCATATACAGTATGATATGATATGATATGATATGAT	360
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Db	361	ATCTTGCTTTCTAATGGGAATATTAACACAATCTGGATCCAAAGATGTGAGAACTA	420
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Db	421	GAAGAAAAATATTAAGAAATTTTTCGAGAGTTTGTACATATTTGTCCAATGTTCA	480
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Db	181	GAAAGTCTTATTCAATCTATGATCATTTTGATGCTACTTTATATACGAAAGTATGTTCCAC	240
QY	241	CCCACTTTCGAAGGTATACAGCATGTAAGTGCCTTCTCTGGAGCTTTCGAAGTTATTTCCACAT	300
Db	241	CCCACTTTCGAAGGTATACAGCATGTAAGTGCCTTCTCTGGAGCTTTCGAAGTTATTTCCACAT	300
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QY	361	ATCTTGCTCTTCTAATGGGAATATTAACAGATCTGGATGCAAAAGATGTGAGACTAGAG	420
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OY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 11
LOCUS I79220 489 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 4 from patent US 5707616.
ACCESSION I79220
VERSION I79220.1 GI:3207510
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein, K.H., Anderson, D.M., Eisenman, J.R., Fung, V. and Rauch, C.
TITLE Method for treating or preventing gastrointestinal disease with
epithelium-derived T-cell factor
JOURNAL Patent: US 5707616-A 4 13-JAN-1998;
FEATURES
source 1..489
location/Qualifiers
BASE COUNT 162 a 81 c 92 g 154 t
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 5,4e-91;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGAGATTTGGAACACACATTTGAGAGTATTTCCATCCAGTGTACTTACTT 60
Db 1 ATGAGATTTGGAACACACATTTGAGAGTATTTCCATCCAGTGTACTTACTT 60
OY 61 CTAAGATCAATTTCTTAACGACCTGGCATTCATGTCCTTCAATTTGGGCTGTTCACT 120
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OY 421 GAAAAAATATTAAGATATTTTGCAGAGTTTGTACATATATGTCCTCAATGTTCAAC 480
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OY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 12
LOCUS CAU03099 1275 bp mRNA linear PRI 25-MAY-1994
DEFINITION Cercopithecus aethiops simian interleukin 15 mRNA, complete cds.
ACCESSION U03099
VERSION U03099.1 GI:493521
KEYWORDS
SOURCE African green monkey.
ORGANISM Cercopithecus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
REFERENCE 1 (bases 1 to 1275)
AUTHORS Grabstein, K.H., Eisenman, J., Shanebeck, K., Rauch, C., Srinivasan, S.,
Johnson, L., Alderson, M.R., Watson, J.D., Schoenborn, M.A., Ahdieh, M.,
Fung, V., Beers, C., Richardson, J., Schoenborn, M.A., Ahdieh, M.,
Cloning of a T cell growth factor that interacts with the beta
chain of the interleukin-2 receptor
JOURNAL Science 264, 965-968 (1994)
MEDLINE 94233380
REFERENCE 2 (bases 1 to 1275)
AUTHORS Anderson, D.M.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1993) Dirk M. Anderson, Immunex Research and
Development Corp., 51 University St., Seattle, WA 98101, USA
FEATURES
source 1..1275
location/Qualifiers
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Query Match 100.0%; Score 489; DB 9; Length 1275;
Best Local Similarity 100.0%; Pred. No. 4,5e-91;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGAGATTTGGAACACACATTTGAGAGTATTTCCATCCAGTGTACTTACTT 60
Db 484 ATGAGATTTGGAACACACATTTGAGAGTATTTCCATCCAGTGTACTTACTT 543
OY 61 CTAAGAGCATTTTCTAATGAGCTGCAATTCATGCTTCAATTTGGGCTGTTCACT 120
Db 544 CTAAGAGCATTTTCTAATGAGCTGCAATTCATGCTTCAATTTGGGCTGTTCACT 603
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variation 119
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BASE COUNT 179 a 93 c 105 g 182 t

ORIGIN

Query Match 99.0%; Score 484.2; DB 9; Length 559;
Best Local Similarity 99.4%; Pred. No. 5.1e-90;
Matches 486; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ATGAGATTTCGAACACCATTTGAGAAATATTCATCCAGTGGTACTGTTTACTT 60
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DB 28 ATGAGATTTCGAACACCATTTGAGAAATATTCATCCAGTGGTACTGTTTACTT 87
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OY 61 CTAAGAGTCATTTCTAATCTAGTGCATTCATGCTTCATTTTGGCTGTTTCACT 120
|||||
DB 88 CTAAGAGTCATTTCTAATCTAGTGCATTCATGCTTCATTTTGGCTGTTTCACT 147
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OY 121 GCAGGGCTCCCTAAACAGAACCACTGGTGATGTATTAAGTATTTGAAAAAATT 180
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DB 148 GCAGGGCTCCCTAAACAGAACCACTGGTGATGTATTAAGTATTTGAAAAAATT 207
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OY 181 GAAGATCTTATTCATCTATGATATTTGCTACTTTTATACAGAAAGTATGTTTCA 240
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DB 208 GAAGATCTTATTCATCTATGATATTTGCTACTTTTATACAGAAAGTATGTTTCA 267
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OY 241 CCCAGTTCGAGGTAACAGCAATGAAGTGCTTCTCTGGAGTGCAGATATTTTCACT 300
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DB 268 CCCAGTTCGAGGTAACAGCAATGAAGTGCTTCTCTGGAGTGCAGATATTTTCACT 327
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OY 301 GAGTCGGAGATACAGATATTCATGATACAGTAAATCTATGATCTAGCAAAACAC 360
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DB 328 GAGTCGGAGATACAGATATTCATGATACAGTAAATCTATGATCTAGCAAAACAC 387
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OY 361 ATCTTGCTTCTAATGGGAATATTAACAGATCTGATGCAAGAAATGTAGAGACTAGAG 420
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DB 388 ATCTTGCTTCTAATGGGAATATTAACAGATCTGATGCAAGAAATGTAGAGACTAGAG 447
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OY 421 GAAAAAATATTTAAAGATTTTTCAGAGTTTGTACATATTTGCCAAATGTTTCAAC 480
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DB 448 GAAAAAATATTTAAAGATTTTTCAGAGTTTGTACATATTTGCCAAATGTTTCAAC 507
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OY 481 ACTTCTTGA 489
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DB 508 ACTTCTTGA 516

RESULT 15
LOCUS AR004268 489 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 4 from patent US 5747024.
ACCESSION AR004268
VERSION AR004268.1 GI:3965147
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 489)

AUTHORS Grabstein,K.H. and Widmer,M.B.
TITLE Vaccine adjuvant comprising Interleukin-15
JOURNAL Patent: US 5747024-A 4 05-May-1998.
FEATURES Location/Qualifiers
source 1..489
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BASE COUNT 159 a 79 c 95 g 156 t

ORIGIN

Query Match 95.1%; Score 465; DB 6; Length 489;
Best Local Similarity 96.9%; Pred. No. 4.7e-86;
Matches 474; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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OY 121 GCAGGGCTCCCTAAACAGAACCACTGGTGATGTATTAAGTATTTGAAAAAATT 180
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DB 121 GCAGGGCTCCCTAAACAGAACCACTGGTGATGTATTAAGTATTTGAAAAAATT 180
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OY 181 GAAGATCTTATTCATCTATGATATTTGCTACTTTTATACAGAAAGTATGTTTCA 240
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DB 241 CCCAGTTCGAGGTAACAGCAATGAAGTGCTTCTCTGGAGTGCAGATATTTTCACT 300
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DB 481 ACTTCTTGA 489

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SUMMARIES

Result No.	Score	% Match	length	DB	ID	Description
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3	489	100.0	489	17	AAT49455	Human epithelium d
4	489	100.0	489	17	AAT42242	Simian epithelium d
5	489	100.0	489	17	AAT36534	Simian epithelium d
6	489	100.0	489	19	AA02874	Human epithelium d
7	489	100.0	489	20	AA29480	Human epithelium d
8	489	100.0	489	21	AA290031	Simian interleukin
9	489	100.0	489	21	AA38245	Human epithelium d

10	489	100.0	489	22	AAE57018	Human EGF (neutro-
9	489	95.1	489	16	AAE00526	Human interleukin-
11	465	95.1	489	17	AAE084584	Human IL-15 clone
12	465	95.1	489	16	AAE09455	Simian epithelium
13	465	95.1	489	17	AAE142243	Human epithelium-d
14	465	95.1	489	17	AAE136685	Human interleukin-
15	465	95.1	489	18	AAE58444	Human interleukin-15 cod
16	465	95.1	489	19	AAE23554	Human interleukin-
17	465	95.1	489	19	AAE29479	Simian epithelium
18	465	95.1	489	21	AAE290032	Simian epithelium-
19	465	95.1	489	21	AAE238244	Human interleukin-
20	465	95.1	489	22	AAE14465	Simian EGF (SEPF)
21	465	95.1	489	22	AAE570117	Human EGF (SEPF)
22	465	95.1	489	20	AAE56368	Human IL-15 DNA.
23	465	95.1	489	20	AAE21342	Human low adenosin
24	465	95.1	1202	21	AAE58044	Human interleukin-
25	465	95.1	1202	21	AAE35220	Human adenosine re
26	465	95.1	1202	21	AAE28708	Human IL-15 CDNA.
27	465	95.1	1202	21	AAE21345	Human low adenosin
28	465	95.1	17904	18	AAE79227	Wild-type interlen
29	465	95.1	489	18	AAE97228	Mutant interleukin
30	463.4	94.8	489	18	AAE35223	Human adenosine re
31	457	93.5	489	21	AAE35223	Human low adenosin
32	364.2	74.5	17844	21	AAE21341	Human adenosine re
33	357.6	73.1	1248	21	AAE35219	Human interleukin-
34	357.6	73.1	1248	21	AAE37358	Human interleukin-
35	357.6	73.1	1248	21	AAE37358	Simian interleukin
36	345	70.6	345	16	AAE00525	Human EGF (hEFG) m
37	345	70.6	345	16	AAE57025	Human low adenosin
38	334	68.3	486	21	AAE21344	Human adenosine re
39	334	68.3	486	21	AAE35222	Human interleukin-
40	325.8	66.6	345	16	AAE00527	Human EGF (SEPF)
41	127.2	26.0	14968	21	AAE21343	Human low adenosin
42	127.2	26.0	14968	21	AAE35221	Human adenosine re
43	127.2	26.0	14968	22	AAE14464	Human IL-15 gene a
44	127.2	26.0	14968	22	AAE15838	Human interleukin
45	127.2	26.0	14968	22	AAE15838	

ALIGNMENTS

XX	RESULT	1
AC	AAT00524	
XX	ID	AAT00524 standard; cDNA; 489 BP.
XX	AAT00524;	
XX	02-FEB-1996	(first entry)
XX	Simian interleukin-15 precursor.	
XX	Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss	
KW		
XX	Cebus apella.	
OS		
XX	Key	location/Qualifiers
FH	CDS	1..489
FT		/+tag= a
FT		/note= "claimed"
FT	misc_feature	145..489
FT		/+tag= b
FT		/note= "claimed"
XX		
XX	WO9527722-A.	
PN		
XX	19-OCT-1995.	
PD		
XX	06-APR-1994;	94WO-US03793.
PP		
XX	06-APR-1994;	94WO-US03793.
PR		
XX		
PA	(IMMV) IMMUNEX CORP.	
XX		

"cc Jun 19 09:14:02 2002

us-09-724-841-4.rng

Anderson DM, Eisenman JR, Fung V, Grabstein KH;
Rauch C;
WPI: 1995-373556/48.
P-PSDB: AAR83436.

Isolated DNA encoding polypeptide with mammalian IL-15 activity - which stimulates proliferation and differentiation of T cells, used for treating carcinoma(s), melanomas, etc. and viral infections
Claim 28; Page 26; 48pp; English.

A simian species of IL-15 (sIL-15) was purified and analysed by SDS-PAGE. Bioassay of unstained gel slices indicated IL-15 activity was associated with proteins having mol. wts in the range of 15-17 kDa. The identity of the first 33 AAs of AAR83309. Subsequent sequencing of the cDNA clone obtd. from a simian library provided a sequence encoding the leader sequence and a mature polypeptide AAR83309. The sequence of the N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers for the amplification of IL-15-specific DNA sequences. The first 6 AAs of the N-terminus were used to design one primer. The first AA sequence of the simian mature N-terminus 26-31 were used to design a second primer, a degenerate mixture coding for a posn. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA cells were used as templates. A 92 bp DNA fragment was used as a cDNA insert. probe to screen a portion of a plasmid library contg. the results in the isolation of clone C85. sIL-15 that has an ORF given in AAT00524. AAR83309 is the active polypeptide & AAR83436 is the precursor polypeptide.

Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other:

Query Match
Best Local Similarity 100.0%; Score 489; DB 16; Length 489;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGAGATTTCGAACACATTTGAGAGATTTTCATCCAGTCTCTGCTTTTACTT 60
Db 1 atgagaatttcgaacacatttgagaagttatctccacagtcacccgctgttactt 60
OY 61 CTAAGAGCTATTCTTCACTGAACCTGCGATTTCATTTGGCTGTTTCACT 60
Db 61 cttaagagctattcttcaactgagagtcgcatcaltcctcttggctgttcaagt 60
OY 121 GCAGGCTCTCCCTAAACAGACCACTGGTGAATGTAATAGATTGAAAAAATT 180
Db 121 gcaaggctctccctaaacagacccaactggcgaatgtaataagattgaaaaaatt 180
OY 181 GAAATCTTATTCATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 240
Db 181 gaagatcttattcattcattcattcattcattcattcattcattcattcattc 240
OY 241 CCCAGTTGCAAGCTAACACATGAGAGCTCTCTGCTGAGTTCGCAAGTATTTCAAT 240
Db 241 cccagttgcaagctaacacatgagagctctctgctgagttcgcaagattttcaat 240
OY 301 GAGTCGGGAGATACAGATATTCATGATACAGTAAATCTTATCCTTACAGCAAC 300
Db 301 gagtcgggagatcacgatatcattcattcattcattcattcattcattcattc 300
OY 361 ATCTTGCTCTTAAATGGAATATACAGAACTGATGCAAAAGATGAGCAACTAG 360
Db 361 atcttgctctttaaattggaattatcagaagatcgtgcaaaagatgagcaaac 360
OY 421 GAAAAAATATTAAGAAATTTTTCAGAGTTTGTACATATTTGCAAAATGTTAT 420
Db 421 gaaaaaataataaagaatttttcagagtttgcacatattgtccaaatgtttat 420
OY 421 gaaaaaataataaagaatttttcagagtttgcacatattgtccaaatgtttat 420

OY 481 ACTTCTTGA 489
Db 481 acttcttga 489

RESULT 2

AA084583
ID AA084583 standard; cDNA; 489 BP.

AC AA084583;

DT 04-SEP-1995 (first entry)

DE Simian IL-15 clone C85.sIL-15.

KW Interleukin-15; IL-15; sIL-15; T-cell growth factor;

KW African green monkey; CV-1; antitumor; virucide; ss.

OS Cercopithecus aethiops.

Key

FT CDS

FT Location/Qualifiers

FT 1..489

FT s1g-peptide

FT 1..144

FT mat-peptide

FT 145..486

FT /tag- C

FT /product- mature IL-15

PN ZA9402636-A.

PN 28-DEC-1994.

PN 18-APR-1994;

PN 94ZA-0002636.

PN 18-APR-1994;

PN 94ZA-0002636.

PN (IMNV) IMMUNEX CORP.

PN Anderson DM, Eisenman JR, Fung V, Grabstein KH;

PN Rauch C;

PN WPI: 1995-082473/11.

PN P-PSDB: AAR6926.

PN New purified interleukin-15 - which induces T cell proliferation

PN and differentiation, used for the treatment of tumours and viral

PN infection

PN Disclosure: Page 26; 47pp; English.

PN cDNA generated from PMA-stimulated CV-1/EBNA cells was amplified

PN by PCR using primers based on the N-terminal sequence of simian

PN interleukin-15 (sIL-15). A probe based on an isolated clone was

PN used to screen a plasmid library containing cDNA inserts prepared from

PN CV-1/EBNA poly-A RNA. Clone C85.sIL-15 was isolated that has the

PN ORF given in AA084583.

PN Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other:

Query Match
Best Local Similarity 100.0%; Score 489; DB 16; Length 489;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGAGATTTCGAACACATTTGAGAGATTTTCATCCAGTCTCTGCTTTTACTT 60
Db 1 atgagaatttcgaacacatttgagaagttatctccacagtcacccgctgttactt 60
OY 61 CTAAGAGCTATTCTTCACTGAACCTGCGATTTCATTTGGCTGTTTCACT 60
Db 61 cttaagagctattcttcaactgagagtcgcatcaltcctcttggctgttcaagt 60

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Db      61 ctaaagagtcatttctaactgaagctgcatcattcttcatatttggcgtttcagt 120
OY      121 GCAGGGGCTCCCTAAACAGACCAAGCGGAGATGATATAGATTTGAAAAAAT 180
Db      121 gaagggtccctaaacagcaacgagctgggtgaatgaatgatttgaataaatt 180
OY      181 GAAGATCTTATTCATATGATATGATGCTACTTATATACGAAAGTATGTTTAC 240
Db      181 gaagatcttatcatcatatgcatatgtacttacttatatacagaagtgatgtccac 240
OY      241 CCCAGTTCAGAGTAAACCAATGAAGTCTTCTTCTGAGTTCGACGTTATTCACAT 300
Db      241 cccagttgaaggtatacagaatgaagtgcttcttcttcttgaagttgcaattatccat 300
OY      301 GAGTCCGGGATACAGATTTTCATGATATGATGAGAAATCTATCTAGCAACAC 360
Db      301 gagtcggagatcacagatcttcatgatacagtaagaaatcttaccctcagcaaacac 360
OY      361 ATCTTGCTCTTAATGGAATATTAACAGATCTGATGCAAGAAATGTAGCAACTAGAG 420
Db      361 atcttgctcttcaatgaggaataatacagaatctgagtcgaagaatgtaggaactagag 420
OY      421 GAAAAAATATTAAGCAATTTTTCAGAGTTCATATTCATATTCATATTCATCAAC 480
Db      421 gaaaaaaatattaaagaatttttgcagaggtttgtacatattgtccaaatgttccaaac 480
OY      481 ACTTCTTGA 489
Db      481 acttcttga 489

RESULT 3
AAT49456
ID      AAT49456 standard; cDNA; 489 BP.
XX
AC      AAT49456;
XX
DT      11-MAR-1997 (first entry)
XX
DE      Human epithelium derived T cell factor cDNA.
XX
KW      hERT; human IMTLH bone marrow stromal cell line; T-cell; B-cell;
KW      lymphocyte; proliferation; differentiation; gastrointestinal;
KW      HIV infection; human immunodeficiency virus; ss.
XX
OS      Homo sapiens.
XX
FH      Key Location/Qualifiers
FH      CDS 1..489
FH      FT /*tag= a
FT      mat_peptide 145..486
FT      FT /*tag= D
FT      FT /product= hETF
XX
XX      US5574138-A.
XX
PD      12-NOV-1996.
XX
PF      08-MAR-1993; 93US-0031399.
XX
XX      22-FEB-1995; 95US-0393305.
XX      08-MAR-1993; 93US-0031399.
XX      22-APR-1994; 94US-0233606.
XX
PA      (IMNV ) IMMUNEX CORP.
XX
PI      Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI      Rauch C;
XX
XX      WPI; 1996-517923/51.
XX      P-PSDB; AAW09100 AND AAW09101.
XX      New epithelium derived T cell factor - induces proliferation of T

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PT      and B cells, stimulates destruction of tumour and virus-infected
PT      cells and protects against toxicity, partic. for treating intestinal
PT      disease and HIV infection
XX
XX      Claim 1; Fig 2; 35pp; English.
XX
CC      Human ETF (epithelium derived T cell factor) cDNA was isolated by
CC      screening a IMTLH cell cDNA library with a simian ETF probe. The
CC      IMTLH cell line was derived from a stable transformation of a human
CC      bone marrow stromal cell culture with pSV3neo. Mature hERT induces
CC      proliferation and/or differentiation of precursor or mature T cells
CC      and is useful for promoting long-term in vitro culture of
CC      T-lymphocytes and T-cell lines. It is used for treating
CC      gastrointestinal diseases including peptic ulcer, colitis and
CC      malignancy and for treating HIV infection.
XX
SQ      Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match      100.0%; Score 489; DB 17; Length 489;
Best Local Similarity 100.0%; Pred. No. 3.3e-116;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 ATGAGATTTGGAACCAATTTGAGAAGTATTTCCATCCAGTCTGTTTACTT 60
Db      1 atgagaatttcgaacacacattgagaagatttccatccagtgctacccgtgttactt 60
OY      61 CTAAGAGTCATTTTCATGATGAGTCAATGATGATGATGATGATGATGATGATGAT 120
Db      61 ctaaaagatcatttctaactgaagctgcatcattcattcattcattcattcattcatt 120
OY      121 GCAGGGGCTCCCTAAACAGACCAAGCGGAGATGATATAGATTTGAAAAAAT 180
Db      121 gcagggtccctaaacagcaacgagctgggtgaatgaatgatttgaataaatt 180
OY      181 GAAGATCTTATTCATATGATATGATGCTACTTATATACGAAAGTATGTTTAC 240
Db      181 gaagatcttatcatcatatgcatatgtacttacttatatacagaagtgatgtccac 240
OY      241 CCCAGTTCAGAGTAAACCAATGAAGTCTTCTTCTGAGTTCGACGTTATTCACAT 300
Db      241 cccagttgaaggtatacagaatgaagtgcttcttcttcttgaagttgcaattatccat 300
OY      301 GAGTCCGGGATACAGATTTTCATGATATGATGAGAAATCTATCTAGCAACAC 360
Db      301 gagtcggagatcacagatcttcatgatacagtaagaaatcttaccctcagcaaacac 360
OY      361 ATCTTGCTCTTAATGGAATATTAACAGATCTGATGCAAGAAATGTAGCAACTAGAG 420
Db      361 atcttgctcttcaatgaggaataatacagaatctgagtcgaagaatgtaggaactagag 420
OY      421 GAAAAAATATTAAGCAATTTTTCAGAGTTCATATTCATATTCATATTCATCAAC 480
Db      421 gaaaaaaatattaaagaatttttgcagaggtttgtacatattgtccaaatgttccaaac 480
OY      481 ACTTCTTGA 489
Db      481 acttcttga 489

RESULT 4
AAT42242
ID      AAT42242 standard; DNA; 489 BP.
XX
AC      AAT42242;
XX
DT      05-FEB-1997 (first entry)
XX
DE      Simian epithelium-derived T cell factor gene.
XX
KW      Epithelium-derived T-cell factor; simian; human; culture; proliferation;
KW      epithelial cell; differentiation; T-lymphocyte; African green monkey;
KW      primer; PCR; polymerase chain reaction; amplification; probe; ss.

```

OS	Cercopithecus aethiops.
XX	
FH	Key
FT	Location/Qualifiers
FT	Sig_peptide
FT	1..144
FT	/tag= a
FT	mat-peptide
FT	145..486
XX	
XX	/tag= b
PN	US5552303-A.
XX	
PD	03-SEP-1996.
PF	
XX	
PR	08-MAR-1993; 93US-0031399.
XX	
PA	(IMMUNEX CORP.
XX	
Pt	Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;
DR	WPI: 1996-412063/41.
XX	P-PsDB: AAM07254.
PT	New isolated simian and human epithelium-derived T-cell factors -
XX	which stimulate the proliferation and/or differentiation of
PS	T-lymphocytes and T-cell lines
XX	
PS	Claim 21; Column 19-20; 22pp; English.
XX	
CC	This is the nucleotide sequence encoding a simian epithelium-derived
CC	T-cell factor (ETF). The protein was purified from African green monkey
CC	CV-1 kidney cells in culture by conventional chromatography: hydrophobic,
CC	anion exchange and reverse phase HPLC, followed by separation by
CC	SDS-PAGE. The proteins from the SDS-PAGE were transferred to a PVDF
CC	membrane and the band corresp. to ETF was cut out for peptide sequencing.
CC	Primers were synthesized based on this sequence and used to amplify a
CC	92 bp fragment from cDNA derived from CV-1/EbNA cells stimulated to
CC	proliferate by phorbol 12-myristate 13-acetate. The 92 bp fragment was
CC	labelled and used as a probe to isolate a clone C85.surf which contained
CC	this sequence. ETF is a protein of 15-17 kd which is expressed by
CC	epithelial cells and stimulates proliferation and/or differentiation of
CC	precursor and/or mature T cells. The protein is therefore useful for
CC	promoting long term in vivo culture of T-lymphocytes and T-cell lines.
XX	
XX	Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;
Query Match	100.0%; Score 489; DB 17; Length 489;
Best Local Similarity	100.0%; Pred. No. 3.3e-116;
Matches 489; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	1 ATGACAATTTGGAACCCACATTGTGAGAACATATTTCCATCGACGTACTACGTGTTACTT 60
bB	1 atggaatttcgaaaccacattggagaagtattccatccagcgtcacctggtttactt 60
OY	61 CTAAAGAGCATATTTCTAATCGAGCTGGCATTCATGCTCTCAATTTGGGCTGTTCACT 120
Db	61 cttaaggatcatcttctctaacygaagctggcatcatcaagtcttaatttggtcttccaft 120
OY	121 GCAGGCTCCCTTAATAACAGAACCCAACCTGGTGTAATGTAATAAGTATTGAAAAAATT 180
Db	121 gcaaggctccccttaaabaacgaagcaacctgggygatataagtaatttgaaaaaatl 180
OY	181 GAAGATCTTATTCATCTATGCATATTGATGCTACTTTATATACGAAGAAGTGATTCAC 240
Db	181 gaagatcttatcatcatcatgcatatcatgactactttatatcagaagaatgaltgccac 240
OY	241 CCCAGTTTCAAGGTAAACAGCAATGAAGAGCTTTCCTTGAGATGGCAACTTATTTACAT 300
Db	241 ccceagttgcaaggtacaagcaatgaagtgcttccctctggagttcgaaagtattatccat 300
OY	301 GAGTCCGGAAGATACGATATTCATGATACAGTAGAAAATCTTATGATCCTAGCAAAACAC 360

Df	301	gattccggagatccaatatactcatgatcagtagaaatcttcaatccacgaacaac	360
Oy	361	AATGTCGCTTCAATGGGAATTATAACGAATCTCGAGTCAAGAATGTGAGAACTAGAG	420
Df	361		420
Oy	421	AAAAAATTTAAAGAAATTTTTGCAGAGTTTTGTCATATTGCCAAAATGTCATCAAC	480
Df	421	gaaaaaatatctaagaatatlttcgcagagtgttgatcatactgtgccaaaatgtcatcaac	480
Oy	481	ACTTCTTGA	489
Df	481	acttcttga	489
 RESULT 5 AAT36634 ID AAT36634 standard; CDNA: 489 BP.			
XX	AAT36634;		
XX	17-NOV-1996 (first entry)		
Dr	Simian interleukin-15 cDNA.		
DE	Interleukin-15; antagonist; mutein; graft versus host disease; allograft; T-cell growth factor; ss. Unspecified simian.		
OS	WO9626274-A1.		
PN	29-AUG-1996.		
PD	21-FEB-1996; 96MO-US02520.		
PF	22-FEB-1995; 95US-0392317.		
PR	(IMKV) IMMUNEX CORP.		
PA	Grabstein KH, Paxton RJ, Pettit DK;		
XX	WPI: 1996-402367/40.		
DR	P-PsDB; AAR98526.		
XX	Antagonists of Interleukin-15 - are used to treat patients having PT symptoms of graft-versus-host disease and for prolonging allo:graft PT survival		
XX	Disclosure: Page 24: 32pp; English.		
XX	A cDNA clone (AAT36634) codes for simian interleukin-15 (IL-15) (AAR98526), a T-cell growth factor. Muteins of simian IL-15 or human IL-15 (see also AAR98527) are useful as antagonists of IL-15 CC and can be prepd. by PCR-mediated mutagenesis of the encoding CC sequences. Preferred muteins have amino acid substitutions at CC Asp56 and/or Glu156 of the IL-15 protein that prevent signal CC transduction. They are useful for treating graft-versus-host CC disease and for prolonging allograft survival.		
XX	Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;		
OY	Query Match	100.0%; Score 489; DB 17; Length 489;	
Df	Best Local Similarity	100.0%; Pred. NO. 3.3e-116;	
Matches	489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Df	1 atggaattttcgaaaccacattcgaggagattcttccaccagtgctacctgtttactt	60	
OY	61 CTAAAGACTCATTTTCTACTGAAGCTGGCATTTGCTCTTCATTTGGGCTGTTACGT	120	

Db	61	ctaaaggtcattcttctaactgaagctcgcatccaatgcttcatttggcgtgttcag	120
Qy	121	GCAGGGCTCCCTAAACAGAACGCCAACGTGGGTGAATGTAAATGAATTTGAAAAAAT	180
Db	121	gcagggctccctaacaacagagccaaactgggtggaatgaataagtgatgtgaaaaaatt	180
Qy	181	GAAATCTTATTCATCTATTCGATATTGATGCTACTTTATATACAGAAAGTATGTTCCAC	240
Db	181	gaagatcttattcaatctatgcatatgcatgctacttatacagaagaatgtgttcac	240
Qy	241	CCCGATTGCAGGTAAACAGCAATGAATGCTTCTCTTGAGTTGGCAAGTATTTCACAT	300
Db	241	ccccgtttgcaaggtaacagcaatgaagtgctctctcttggaagtgcaagttatccaat	300
Qy	301	GAGTCGCGAGATACAGATATTTCATGATACAGTAGTGAAGAAATTTATTCATCCTCAGCAAAACAC	360
Db	301	gagtcgcggagataagatattccaatgaatacagtagtgaaaaacttatcatcctcagaaacaac	360
Qy	361	ATCTTGTCCTTAATGGGAATATATACGAATCTGGATGCAAGAAGTGTGAGAACTAGAG	420
Db	361	atcttgctctctaattggaataataacaagaatctggaatgcaagaatgtgsgaactaag	420
Qy	421	GAAGAAATATTTAAAGATTTTTCACAGTTTGTACATATTTGTCCAAATGTTTCATCAC	480
Db	421	gaagaaatatataagaatcttttcagagattttgatacatatgtccaaatgttcataac	480
Qy	481	ACTTCTTGA 489	
Db	481	acttcttga 489	

XX	AAV02874	standard; DNA; 489 BP.
XX	AAV02874;	
XX	08-MAY-1998	(first entry)
XX	Human epithelium derived T-cell factor DNA.	
XX	Epithelium derived T-cell factor; ERF; human; gastrointestinal disease	
XX	B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;	
XX	treatment; prevention; ss.	
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	1..489
FT		/*tag= a
FT		//product= ERF
FT	sig.-peptide	1..144
FT		/*tag= b
FT	mat.-peptide	145..486
FT		/*tag= c
FT		//product= ERF
FT		/note="Epithelium-derived T-cell factor"
XX		
PN	US5707616-A.	
XX		
PD	13-JAN-1998.	
XX		
PF	04-OCT-1996;	96US-0726817.
XX		
XX	22-FEB-1995;	95US-0393305.
PR	08-MAR-1993;	93US-0031399.
PR	22-APR-1994;	94US-0233606.
XX		
PA	(IMMV) IMMUNEX CORP.	
XX		
PI	Anderson DM, Eisenman JR, Fung V, Grabstein KH;	
PI	Rauch C;	

XX	WPI: 1998-100295/09.
DR	P-PsDB: AAW39187.
XX	
PT	Treatment or prevention of gastrointestinal diseases - by
PT	administering epithelium-derived T-cell factor polypeptide
PS	
XX	Claim 1C; Column 37-40; 34pp; English.
CC	
CC	This sequence encodes a human epithelium-derived T-cell factor (ETF)
CC	which is used in a method for treating or preventing gastrointestinal
CC	disease. These polypeptides have particular application in the treatment
CC	of gastrointestinal disorders associated with disruption of the
CC	gastrointestinal epithelium or villi such as chemotherapy- and
CC	radiation-therapy induced enteritis (gut toxicity), mucositis, peptic
CC	ulcer disease, gastroenteritis and colitis, villus atrophic disorders,
CC	malignancy and inflammatory bowel disease. ETF polypeptides may also be
CC	useful in the treatment of human immunodeficiency virus (HIV) and
CC	HIV-associated disease due to their ability to stimulate CD4+ and CD8+
CC	cells. Biologically active ETF may be used to treat a variety of other
CC	diseases or conditions where T-cell or B cell stimulation is desired.
SO	
XX	Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other:
Query Match	100.0%; Score 489; DB 19; Length 489;
Best Local Similarity	100.0%; Pred. No. 3.3e-116;
Matches 489; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 ATGAGAAATTTCGAACACCACATTTGGAGAAGTATTTCCATCGACGTCTGTTACTT 60
Db	1 atgagaatttcgaaccacacatltggaaagtatltccatccagtgctactgtgttacct 60
OY	61 CTAAAGATCATATTTCTTAACGTAAGCTGCATTCATGCTTCATTTTGSGCTGTTCACT 120
Db	61 ctaaagatcatattttctaactgaagctgcattcatcatttcttattggtcglttcagt 120
OY	121 GCAGGCGTCCCTAAAACAGAACGCCAAGTGGGTAATGTAATAAGTATTTGAAAAAATT 180
Db	121 gccaggctcccctaaaacagaagccaactgggtagaatgataaagtgatltgaaaaaatt 180
OY	181 GAAGATCTTATTCATCTGTGCATATTTGATGAGTACTTTTATACAGAAAGTGATGTTTAC 240
Db	181 gaagactcttatccaactctatgatcatatgtatgtcctactttatatcacagaagtgatgtcc 240
OY	241 CCCAGTTGCAAGGTAACAGCAATGAAGTGTCTTCTTGAGTTCGAAGTTATTTTACAT 300
Db	241 ccagttgcaaggtaacacgaatgaagtgcttctctctgtgagtgtaagttattacaat 300
OY	301 GACTCGGGAATCACATATTTTCATGTATACGTGAAATCTTATTCACGTCAGCAACAAC 360
Db	301 gactccgggaatcacatatvtttcatgtatpacgtgaaatcttatttcacgccagcaacaac 360
OY	361 ATCTTGCTTTCTAATGGAATATACAGAAATCTGATGCAAGAAATGTGAGAACTAGAG 420
Db	361 atcttgtctttaatggaaatacaagaatctgtagtcaagaatcgttggagacagag 420
OY	421 GAAAAAAATTTAAAGATTTTGCAGAGTTTGTACATATTCACAAATGTCATCAAC 480
Db	421 gaaaaaaatattaagaatlttcgacagatcttgtaacatatgtccaatgltcatcaaac 480
OY	481 ACTTCTTTGA 489
Db	481 acttcttga 489
RESULT	7
AAAX29480	
ID	AAAX29480 standard; DNA: 489 BP.
XX	
XX	AAAX29480;
XX	
DT	10-JUN-1999 (first entry)

Db	181	gaagatcttatttcaatctatgcataatgtacttattatatacagaagtgatgttcac	240
Oy	241	CCGAGTTGCAAGTAAACAGCAATGAAGTGGCTTCTCTTGGAGTGAAGTTATTTCACAT	300
Db	241	ccccagttgcgaagtgataacagagaatgagtgcttcttcttgagtgcaagttatttcacat	300
Oy	301	GAGTCCGGAGATACAGATATTTCATGATACAGTGAAGAAATCTTATCATCTAGCAAAAC	360
Db	301	gagtcctcgagatcacagatattcatgcagtagaataatcttacccttagcaacaac	360
Oy	361	ATCTGTCTTCTTATGAGGAATTAAACGAATCTGAGANGCAAGAAATGTCAGGAAC	420
Db	361	atctgtcttcttctatctggaataataacagatccgagatgcaagaatgctggaactagag	420
Oy	421	GAAGAAATATTAAAGAAATTTTGCAGAGCTTTTGTACATATTGTCCAAATGTTTCATCAC	480
Db	421	gaaaaaataatataaagaattttcgcagagtttctacatatgtccaaatgttcatcaac	480
Oy	481	ACTTCTTGA	489
Db	481	acttcttga	489
Db	481	acttcttga	489

RESULT 8
 AAZ90031
 ID AAZ90031 standard; cDNA; 489 BP.
 AC AAZ90031:
 AT 09-MAY-2000 (first entry)
 DE Simian interleukin-15 (IL-15) nucleotide sequence.
 KW Interleukin-15; IL-15; antagonist; irritable bowel disease; IBD;
 KW celiac disease; treatment; ss.
 OS Primate.
 PN WO200002582-A2.
 PD 20-JAN-2000.
 XX 09-JUL-1999; 99WO-GB02201.
 XX 10-JUL-1998; 98GB-0014892.
 PA (KENN-) KENNEDY INST RHEUMATOLOGY MATHILDA & TER.
 PI Londei M, Quarantino S, Maiuri L;
 DR WPI: 2000-171080/15.
 DR P-PSDB: AAY78594.
 PT Use of antagonists of interleukin-15 for treating an inflammatory bowel
 XX disease, particularly celiac disease
 PS Disclosure: Page 70; 70pp; English.
 CC This sequence represents the simian interleukin 15 (IL-15) nucleotide
 CC sequence. The IL-15 nucleotide sequence and the protein encoded by it can
 CC be used to determine and create antagonists of IL-15. An antagonist of
 CC IL-15 can be used for treating an inflammatory bowel disease (IBD). The
 CC invention relates to the treatment of celiac disease using IL-15
 CC antagonists. The antagonists are preferably mutants of IL-15, antibodies
 CC against IL-15 or IL-15 molecules bound to chemical groups that interfere
 CC with the ability of IL-15 to effect a signal transduction through either
 CC the alpha or the gamma subunit of the IL-15 receptor complex. The IL-15
 CC antagonists of the invention can be used to treat irritable bow disease
 CC especially celiac disease.
 XX Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match 100.0%; Score 489; DB 21; Length 489;
 Best Local Similarity 100.0%; Pred. No. 3.3e-116;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTTGCAACACATTTGAGAGTATTTCCATCCAGTGTCTACTTGTACTT 60
 |||||||
 Db 1 atggaatttcgaacacacatttgaagaatttccaccagctgtacctgttacct 60

QY 61 CTAAGAAGTCATTTTCACTGAAGTCGATTCATGCTTCATTTTGGCGTTTCAGT 120
 |||||||
 Db 61 ctaaagagtcatttctcaactgaagctggcaltcatgtcttcttcttggctgttcagt 120

QY 121 GCAGGGCTCCCTAAACAGAACCCAGCTGGGTGATGATATAGTGAATTTGAAAAAATT 180
 |||||||
 Db 121 gcagggtcccttaaacagaagccaactgggtgataatgaatgtatttgaaaaaatt 180

QY 181 GAAGATCTTATTCATATGATATGATGATGCTTATTTATACAGAAAGTGTTCAC 240
 |||||||
 Db 181 gaagatcttattcatctatcatatgatacttacttatacagaagtgatgttcac 240

QY 241 CCCAGTTGCAAGTACAGCAATGAGTCTTCTGTTGAGTGGCAAGTATTTTCACAT 300
 |||||||
 Db 241 cccagttgcaaggaagaaacagcaatgaatgtcttcttcttggagtgcaagtattcacat 300

QY 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCATCTAGCAAAACAC 360
 |||||||
 Db 301 gagtcggagatacagatatctatcatgatacagtagaataatctatcatctctgcaaaacac 360

QY 361 ATCTTGCTTCTATGGAATATACAGATCTGATGCAAAAGATGTGAGGAAGTACAG 420
 |||||||
 Db 361 atcttgcttctaatggaataataacagaaatctgatacgaagatggaagaaactagag 420

QY 421 GAAAAAATATTAAGAATTTTTCAGAGTCTTGTACATATTTGCCAATGTTCATAC 480
 |||||||
 Db 421 gaaaaaataataagaatttttgcagagtttgcagatttgcacataatgccaaatgttcatcac 480

QY 481 ACTTCTTGA 489
 |||||||
 Db 481 acttcttga 489

RESULT 9
 AAZ38245
 ID AAZ38245 standard; CDNA; 489 BP.
 XX
 AC AAZ38245;
 XX
 DT 09-FEB-2000 (first entry)
 XX
 DE Human epithelium-derived T-cell factor (ETF) CDNA.
 XX
 KW ETF: epithelium-derived T-cell factor; T-cell; T-lymphocyte;
 KW proliferation; differentiation; growth factor; precursor; mature; CD4+;
 KW CD8+; gastrointestinal; epithelium; cell culture; treatment; HIV;
 KW gastrointestinal disease; gastroenteritis; colitis;
 KW inflammatory bowel disease; villus atrophic disorder; enteritis;
 KW chemotherapy; radiotherapy; gut toxicity; cancer; side effect;
 KW tolerated dose; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..489
 FT /*tag= a
 FT /product= "Human ETF precursor protein (AAV52310)"
 FT 1..144
 FT sig_peptide
 FT /*tag= b
 FT 145..489
 FT /*tag= c
 FT /product= "Mature human ETF (AAV52311)"
 XX
 XX US5985262-A.
 PN

PD 16-NOV-1999.
 XX
 PF 03-FEB-1997; 97US-0794524.
 XX
 PR 22-FEB-1995; 95US-0393305.
 PR 04-OCT-1996; 96US-0726817.
 PR 08-MAR-1993; 93US-0031399.
 PR 22-APR-1994; 94US-0233606.
 XX
 PA (IMM) IMMUNEX CORP.
 XX
 PI Rauch C, Fung V, Eisenman JR, Grabstein KH, Anderson DM;
 DR WPI: 2000-022267/02.
 DR P-PSDB: AAV52310, AAV52311.
 XX
 XX Stimulation of T-cells in human immunodeficiency virus infected
 PT patients -
 PS Claim 1; Columns 37-40; 33pp; English.

This sequence represents human epithelium-derived T-cell factor (ETF) CDNA. ETF is a previously unidentified T-cell growth factor which stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to proliferate and differentiate. It also promotes proliferation of the gastrointestinal epithelium. The protein can be used to promote long-term in vitro culture of T-lymphocytes and T-cell lines. ETF can be used for treating HIV infection, HIV-associated diseases, and other diseases or conditions where stimulation of T-cell proliferation would be desirable e.g., it could be used to augment the destruction of tumour cells or virally-infected cells. ETF may also be used to treat or prevent gastrointestinal disease, including chemotherapy and radiotherapy associated enteritis, gastroenteritis, colitis, inflammatory bowel disease and villus atrophic disorders. Chemotherapy and radiotherapy associated enteritis (gut toxicity) results in bleeding and sepsis due to gastrointestinal flora entering the blood, and thus can limit the dosage of therapeutic agent administered to a cancer patient. ETF may therefore be used to increase the tolerated doses radiotherapy and chemotherapy.

Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match 100.0%; Score 489; DB 21; Length 489;
 Best Local Similarity 100.0%; Pred. No. 3.3e-116;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTTGCAACACATTTGAGAGTATTTCCATCCAGTGTCTACTTGTACTT 60
 |||||||
 Db 1 atggaatttcgaacacacatttgaagaatttccaccagctgtacctgttacct 60

QY 61 CTAAGAAGTCATTTTCACTGAAGTCGATTCATGCTTCATTTTGGCGTTTCAGT 120
 |||||||
 Db 61 ctaaagagtcatttctcaactgaagctggcaltcatgtcttcttcttggctgttcagt 120

QY 121 GCAGGGCTCCCTAAACAGAACCCAGCTGGGTGATGATATAGTGAATTTGAAAAAATT 180
 |||||||
 Db 121 gcagggtcccttaaacagaagccaactgggtgataatgaatgtatttgaaaaaatt 180

QY 181 GAAGATCTTATTCATATGATATGATGATGCTTATTTATACAGAAAGTGTTCAC 240
 |||||||
 Db 181 gaagatcttattcatctatcatatgatacttacttatacagaagtgatgttcac 240

QY 241 CCCAGTTGCAAGTACAGCAATGAGTCTTCTGTTGAGTGGCAAGTATTTTCACAT 300
 |||||||
 Db 241 cccagttgcaaggaagaaacagcaatgaatgtcttcttcttggagtgcaagtattcacat 300

QY 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCATCTAGCAAAACAC 360
 |||||||
 Db 301 gagtcggagatacagatatctatcatgatacagtagaataatctatcatctctgcaaaacac 360

QY 361 ATCTTGCTTCTATGGAATATACAGATCTGATGCAAAAGATGTGAGGAAGTACAG 420
 |||||||
 Db 361 atcttgcttctaatggaataataacagaaatctgatacgaagatggaagaaactagag 420

CC	Lymphocytes, to augment anti-infectious disease immunity, to induce CTL,
CC	LAK or NK lytic activity, or to augment the destruction of tumour cells
CC	or cells infected with virus. The present sequence represents a cDNA
CC	encoding the human E7F (here) polypeptide.
xx	
SQ	Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;
Query Match	100.0%; Score 489; DB 22; Length 489;
Best Local Similarity	100.0%; Pred. No. 3.3e-116;
Matches 489; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 ANGACAATTTCGAACCAACCATTTGAGAGTATTCACATCCACTGGCTGCTTACTT 60
DB	1 aagagaatttcgaaaccaaatcttgaggaaatcctccacagtgctaaccgtgttacct 60
OY	61 CTAAAGAGTCATATTTCTAAGTAAGTGAACGTGCATTCATGCTTATTTTGCGCTGTTCACT 120
DB	61 cttaagaagcatctttcctaacttgaagctgcatcatactgcattcatttggcgcttcagt 120
OY	121 GCAGGCGCTCCATAAACAGAGCCAACCTGGTGGAATGTAATAGTATTGAAAAAATT 180
DB	121 gcaagggtcccctaaaacagaagccaactgytgaaatgataagtgatttgaaaaaalt 180
OY	181 GAAGAATCTTATTCATCTATGATATTTGATGCTACTTTTATACGAAGAAAGTATGTCAC 240
DB	181 gaagatcttatccaatcatactgatcatatgtagtctaactttatacagaagaatgagtgltcac 240
OY	241 CCCACTTGGCAAGGTAAACAGCAATGAAGTGCCTTCTCTTGAGACTTGCAAGTATTTACAT 300
DB	241 cccagtttgaaggtacaacgaatgaagtgcttcttccttgaggttcgaagtatttcacact 300
OY	301 GAGTCGCGAGATACAGATATTTGATGATACAGTAGAAAATCTTATGATCCTAGCAAAACAC 360
DB	301 gagtcgcgagatacagatatcatgatagacagtagaanaatcttatcatctctagcaaacac 360
OY	361 ATCTGTCTCTTAATGCGAATATTAACAGATTTGTGATGGAAGATGTGAGACTAGAG 420
DB	361 atctgtctcttaagtgagataaacagatcttgatgaaagaatlgtaggaactaag 420
OY	421 GAAAAAATATTAAGAATTTTTGAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480
DB	421 gaaaaaataataaagaattttgcagagtttgttaacatatgtgccaaaatgttcatcaac 480
OY	481 ACTTCTTGA 489
DB	481 acttcttga 489
RESULT 11	
AAT00526	
ID	AAT00526 standard; cDNA; 489 BP.
XX	
NC	AAT00526;
XX	
DT	02-FEB-1996 (first entry)
XX	
DE	Human interleukin-15 precursor.
XX	
KX	Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.
XX	
OS	Homo sapiens.
XN	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..489
FT	/tag= "a"
FT	/note= "Claimed"
FT	misc_feature
FT	145..489
FT	/tag= b
FT	/note= "claimed"
PN	W09527722-A.
XX	

PD 19-OCT-1995.
 XX 06-APR-1994; 94WO-US03793.
 PF 06-APR-1994; 94WO-US03793.
 PR 06-APR-1994; 94WO-US03793.
 XX
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 PI Rauch C;
 XX
 DR WPI: 1995-373556/48.
 P-PSDB: AAR83438.
 XX
 PT Isolated DNA encoding polypeptide with mammalian IL-15 activity - which
 PT stimulates proliferation and differentiation of T cells, used for
 PT treating carcinoma(s), melanomas, etc. and viral infections
 XX
 PS Claim 36, Page 28-29; 48pp; English.
 XX
 CC A simian species of IL-15 (sIL-15) was purified and its AA
 CC sequence and cDNA sequence analysed (see AAR83309, AAR83436,
 CC AAT00524, AAT00525). Both the simian and the human ORFs encode
 CC a precursor polypeptide (AAR83436, AAR83438). The precursor
 CC polypeptides each comprise a 48-AA leader sequence and a sequence
 CC encoding mature simian or human IL-15 polypeptides. The active
 CC simian and human IL-15 polypeptides are disclosed in AAR83309 &
 CC AAR83310 respectively. The invention also comprises other mammalian
 CC IL-15, including human IL-15, that hybridise to probes defined by
 CC AAR83438. A plasmid contg. a recombinant clone of human IL-15
 CC cDNA was deposited with ATCC on Feb. 19 1993 under ATCC 69245.
 CC The deposit was named 141-hETF. AAR83435 is a mammalian mature
 CC IL-15 polypeptide. It is a generic sequence which encompasses both
 CC AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.
 XX
 XX
 SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 95.1%; Score 465; DB 16; Length 489;
 Best Local Similarity 96.9%; Pred. No. 4.8e-110;
 Matches 474; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 1 ATGAGAAATTTGGAACCAACATTTGAGAGATTTCCATTCAGTCTGCTGCTTACTT 60
 Db 1 atgagaatttcgaacacacattgagaagtattccatccagctctacttggtttactt 60
 OY 61 CTAAGAGTCAATTTCTAACTGAAGCTGGCATGCTCTTCATTTGGGCTGTTTCAGT 120
 Db 61 ctaaacagctatttctaactgaagctggcatctgcttcatcttggctgttcagt 120
 OY 121 GCAGGGCTCCCTAAACAGAACCCACCTGGGTAATGTAAAGTGATTTGAAAAAATT 180
 Db 121 gcagggtctcttaaacagaaagccaactgggtgaatgaataagattgaaaaaaatt 180
 OY 181 GAAGATCTTATTCATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Db 181 gaagatcttattcaatcatcatgacatgactgacttataatacgaagaagtgatgtaac 240
 OY 241 CCCAGTTCAGAGTAACAGCAATGAAGTCTTCTCTTGAGTTGCAAGTTATTTACAT 300
 Db 241 cccagttgcaagtaagtaacagcaatgaagtgcttctcttgagttgcaagttatttacc 300
 OY 301 GAGTCGGAGATACGATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 Db 301 gagtcggagatgacgattcatgacatgacatgacatgacatgacatgacatgacatgac 360
 OY 361 ATCTTGTCTTCTAATGGAATATTAACAGATCTGATGCAAGATGTCAGCACTAGAG 420
 Db 361 agttgtcttctcaatggaatgtaacagatctgagtgcaagaatgtaagaactggag 420
 OY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGTCCAAATGTTTCATC 480
 Db 421 gaaaaaataatataagaatttttgcagagtttgtacatattgtccaaatgttcatcaac 480

OY 481 ACTTCTTGA 489
 Db 481 acttcttga 489

RESULT 12
 AAQ84584
 ID AAQ84584 standard; cDNA; 489 BP.
 XX
 AC AAQ84584;
 XX
 DT 04-SEP-1995 (first entry)
 XX
 DE Human IL-15 clone 141.hETF.
 XX
 KW Interleukin-15, IL-15, hIL-15; T-cell growth factor;
 KW antitumor; virucide; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..489
 FT /tag= a
 FT /product= IL-15 precursor
 FT sig-peptide 1..144
 FT /tag= b
 FT mat-peptide 145..486
 FT /tag= c
 FT /product= mature IL-15
 XX
 PN ZA9402636-A.
 XX
 PD 28-DEC-1994.
 XX
 XX 18-APR-1994; 94ZA-0002636.
 XX
 PR 18-APR-1994; 94ZA-0002636.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 PI Rauch C;
 XX
 DR WPI: 1995-082473/11.
 P-PSDB: AAR66927.
 XX
 PS Disclosure: Page 28-29; 47pp; English.
 XX
 CC A sIL-15 probe was prepared from isolated simian interleukin-15
 CC cDNA and used to screen a cDNA library generated from the IMTLH
 CC cell line derived from human bone marrow stromal cells. Clone
 CC 141.hETF encoded human IL-15.
 XX
 SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 95.1%; Score 465; DB 16; Length 489;
 Best Local Similarity 96.9%; Pred. No. 4.8e-110;
 Matches 474; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 1 ATGAGAAATTTGGAACCAACATTTGAGAGATTTCCATTCAGTCTGCTGCTTACTT 60
 Db 1 atgagaatttcgaacacacattgagaagtattccatccagctctacttggtttactt 60
 OY 61 CTAAGAGTCAATTTCTAACTGAAGCTGGCATGCTCTTCATTTGGGCTGTTTCAGT 120
 Db 61 ctaaacagctatttctaactgaagctggcatctgcttcatcttggctgttcagt 120

Query Match	Best Local Similarity	Score	DB	Length	489;
Matches	4/74; Conservative	0; Mismatches	15; Indels	0; Gaps	0;
0Y	1	ATGAGATTTCGAAACACACATTTGAGAGATTTCCATCCAGTCCAGTCTGTTACTT	60		
Db	1	atgagaatttcgaacacacattggaagtattccattccacagtgctactggttactt	60		
0Y	61	CTAAAGAGTCATTTTCTAATCTGACGTGGCATTCATGTCTTCATTTTGGCTGTTCACT	120		
Db	61	ctaaacagtcatttcttaactcgaagctgycattcattccttcatcttggccttcagtt	120		
0Y	121	GCAGGCGTCCCTAAACAGAACCCAACTGGGCTGATGTAAATGATGATTGAAAAAATT	180		
Db	121	gaagggtctcccaaaacagaagccacctgggtgaaatgcaataagtgattgaaaaaat	180		
0Y	181	GAAAGTCTTATTCAATCTATGATATTTGATGCTACTTTATATATACGAAAGTGATGTCAC	240		
Db	181	gaagctctatcacaatcattgcatattgatctacttatacgaagaatgattctac	240		
0Y	241	CCCAATTCGAAAGGTAAACGCAATGAAGGCTTCTCTGAGGTTCCAGTTATTTACAT	300		
Db	241	cocagttgcaaaagtacacgaatgaagtgcttctccctggagttcacaagttattccact	300		
0Y	301	GAGTCCGAGATACGATATTTCTATGATACAGTAGAAAACTTATCATCTAGCAAAACAC	360		
Db	301	gagtcggaagatgcagaattcatcattacagtagaanaatcgtatcatccttagcaaacac	360		
0Y	361	ATCTGTTCTTAATGGAAATATATAACAATCTGGATCCAAAGATGTGAGAACTAGAG	420		
Db	361	agttgcttctcctaaagggaatgtaacagaatctggaatgcaagaatgtaagaactgag	420		
0Y	421	GAATAAATAATATTAAGAATTTTTCAGAGCTTTTGACATATTTGCAAAATTTTCATCAC	480		
Db	421	gaaaaaataataagaatttttgcagagttttgacatattgcccacaaatgttcatcaac	480		
0Y	481	ACTTCTTGA 489			
Db	481	actctctga 489			

RESULT 14

AAAT42243

ID AAT42243 standard; DNA: 489 BP.

XX AC AAT42243:

XX 05-FEB-1997 (first entry)

XX DE Human epithelium-derived T cell factor gene.

XX Epithelium-derived T-cell factor; simian; human; culture; proliferation;

KW epithelial cell; differentiation; T-lymphocyte; African green monkey;

primer: PCR: polymerase chain reaction; amplification; probe; ss.
 XX Homo sapiens.

Key Location/Qualifiers
 sig_peptide 1..144
 FT /*tag= a
 FT mat_peptide 145..486
 FT /*tag= b

US5552303-A.

03-SEP-1996.

08-MAR-1993; 93US-0031399.

08-MAR-1993; 93US-0031399.

(IMMV) IMMUNEX CORP.

Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;

WPI: 1996-412063/41.

P-PSDB: AAM07255.

New isolated simian and human epithelium-derived T-cell factors -
 T-lymphocytes and T-cell lines

Claim 21: Column 23-24; 22pp; English.

This is the nucleotide sequence encoding a human epithelium-derived
 T-cell factor (ETF). The gene was obtained using a 1.37 kb fragment of
 the corresp. African green monkey gene (AAT42242) as a probe to screen a
 cDNA library constructed from RNA derived from the IMVH cell line.
 CC This cell line is derived by stable transformation of a human bone
 marrow stromal cell culture with pSVneo. From a pool of about 1000 cDNA
 clones, one clone 141.herb contained this sequence. ETF is a protein of
 15-17 kD which is expressed by epithelial cells and stimulates
 CC proliferation and/or differentiation of precursor and/or mature T cells.
 CC The protein is therefore useful for promoting long term in vivo culture
 of T-lymphocytes and T-cell lines.

Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 95.1%; Score 465; DB 17; Length 489;

Best Local Similarity 96.9%; Pred. No. 4.8e-110;

Matches 474; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAAACACATTTGAGAGATTTTCATCCAGTGTCTGCTGTTTACTT 60
 DB 1 atgagaatttcgaacacacatttgagaagatttcacatccagtgctacttggttactt 60
 QY 61 CTAAGAGTCATTTTCTAATGAGCGGATTCATCTCTTCAATTTGGGCTGTTTACTT 120
 DB 61 ctaaaagtcatttctcaactgaagcggatcattcaatgctcttggctgttcaagt 120
 QY 121 GCAAGGCTCCCTAAACAGAGCCCACTGGGTGAATTAAGTGAATTTGAAAAAATT 180
 DB 121 gcagggtctctcaaaacagagccaactgggtgaatgtaagtgtttgaaaaaatt 180
 QY 181 GAAGATCTTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 181 gaagatcttttcaatgataatgataatgataatgataatgataatgataatgata 240
 QY 241 CCCAGTTCAAGGTAACAGCAATGAAGTCTTCTCTTGGAGTTGCAAGTATTTTCAAT 300
 DB 241 cccagttcagaagtaacagcaatgaagtgcttctcttggagttacaaagttatctca 300
 QY 301 GAGTCCGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 301 gagtcggagatgcaagattatcatagtagtaagaaatctgataatcctagcaaaaca 360

QY 361 ATCTTGCTCTCTAATGGAATATTAACAGAAATCTGCATCAAGAAATGTGAGCACTAGAC 420
 DB 361 agttgtcttctctaatggaatattgaaacagaaatctgataatgataatgataatgata 420
 QY 421 GAAAAAATATTAAAGCAATTTTGGAGCTTTTACATATTGTCACAAATGTTATCAAC 480
 DB 421 gaaaaaaatataaagaattttgcaaggttttgtaacatattgtccaaatgttcatcaac 480
 QY 481 ACTTCTTGA 489
 DB 481 actcttga 489

RESULT 15

AAT36635

ID AAT36635 standard; cDNA; 489 BP.

AC AAT36635;

DE 17-NOV-1996 (first entry)

DE Human interleukin-15 cDNA.

DE Interleukin-15; antagonist; mutein; graft versus host disease;

KW allograft; T-cell growth factor; ss.

OS Homo sapiens.

PN WO9626274-A1.

XX 29-AUG-1996.

XX 21-FEB-1996; 96WO-US02520.

PR 22-FEB-1995; 95US-0392317.

PA (IMMV) IMMUNEX CORP.

PI Grabstein KH, Paxton RJ, Pettil DK;

XX WPI: 1996-402367/40.

DR P-PSDB: AAR98527.

PT Antagonists of interleukin-15 - are used to treat patients having

PT symptoms of graft-versus-host disease and for prolonging allo:graft

PT survival

PS Disclosure; Page 25; 32pp; English.

XX A cDNA clone (AAT36635) codes for human interleukin-15 (IL-15)

CC (AAR98527), a T-cell growth factor. Muteins of human IL-15 or

CC simian IL-15 (see also AAR98526) are useful as antagonists of IL-15

CC and can be prepd. by PCR-mediated mutagenesis of the encoding

CC sequences. Preferred muteins have amino acid substitutions at

CC Asp56 and/or Gln156 of the IL-15 protein that prevent signal

CC transduction. They are useful for treating graft-versus-host

CC disease and for prolonging allograft survival.

XX

Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 95.1%; Score 465; DB 17; Length 489;

Best Local Similarity 96.9%; Pred. No. 4.8e-110;

Matches 474; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAAACACATTTGAGAGATTTTCATCCAGTGTCTGCTGTTTACTT 60
 DB 1 atgagaatttcgaacacacatttgagaagatttcacatccagtgctacttggttactt 60
 QY 61 CTAAGAGTCATTTTCTAATGAGCGGATTCATCTCTTCAATTTGGGCTGTTTACTT 120
 DB 61 ctaaaagtcatttctcaactgaagcggatcattcaatgctcttggctgttcaagt 120

[illegible]

Search completed: June 19, 2002, 00:56:16
Job time: 2794 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2002, 23:32:52 ; Search time 60.38 Seconds
(without alignments)
1989.314 Million cell updates/sec

Title: US-09-724-841-1

Perfect score: 489
Sequence: 1 ATGAGATTTCGAAACACCA.....TGTTCAACACCTTCTTGA 489

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

Issued Patents_NA: *
1: /cgn2_6/prodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/prodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/prodata/2/ina/6A_COMB.seq: *
4: /cgn2_6/prodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/prodata/2/ina/PCITUS_COMB.seq: *
6: /cgn2_6/prodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	489	100.0	489	1	US-08-031-399-4 Sequence 4, Appli
2	489	100.0	489	1	US-08-393-305-1 Sequence 1, Appli
3	489	100.0	489	1	US-08-535-733-1 Sequence 1, Appli
4	489	100.0	489	1	US-08-726-817-1 Sequence 1, Appli
5	489	100.0	489	1	US-08-504-042-4 Sequence 4, Appli
6	489	100.0	489	1	US-08-392-317B-2 Sequence 2, Appli
7	489	100.0	489	2	US-08-725-969-1 Sequence 1, Appli
8	489	100.0	489	2	US-08-794-524-1 Sequence 1, Appli
9	489	100.0	489	3	US-09-134-132-2 Sequence 2, Appli
10	489	100.0	489	4	US-09-134-134A-2 Sequence 2, Appli
11	489	100.0	489	4	US-09-134-456-2 Sequence 2, Appli
12	489	100.0	489	4	US-09-196-427-2 Sequence 2, Appli
13	489	100.0	489	4	US-09-189-193-1 Sequence 1, Appli
14	489	100.0	489	5	PCT-US94-03793-4 Sequence 4, Appli
15	489	100.0	489	5	PCT-US96-06423-1 Sequence 1, Appli
16	489	100.0	489	3	US-08-962-503-11 Sequence 11, Appli
17	487.4	99.7	489	3	US-08-842-947-5 Sequence 5, Appli
18	481	98.4	489	3	US-08-842-947-7 Sequence 7, Appli
19	465	95.1	489	1	US-08-031-399-1 Sequence 1, Appli
20	465	95.1	489	1	US-08-393-305-4 Sequence 4, Appli
21	465	95.1	489	1	US-08-726-817-4 Sequence 4, Appli
22	465	95.1	489	1	US-08-504-042-1 Sequence 1, Appli
23	465	95.1	489	1	US-08-392-317B-1 Sequence 1, Appli
24	465	95.1	489	2	US-08-725-969-4 Sequence 4, Appli
25	465	95.1	489	2	US-08-794-524-4 Sequence 4, Appli
26	465	95.1	489	3	US-09-134-132-1 Sequence 1, Appli
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28	465	95.1	489	4	US-09-134-456-1 Sequence 1, Appli
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33	345	70.6	345	1	US-08-393-305-12 Sequence 12, Appli
34	345	70.6	345	1	US-08-726-817-12 Sequence 12, Appli
35	345	70.6	345	2	US-08-725-969-12 Sequence 12, Appli
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38	325.8	66.6	345	1	US-08-393-305-13 Sequence 13, Appli
39	325.8	66.6	345	1	US-08-726-817-13 Sequence 13, Appli
40	325.8	66.6	345	2	US-08-725-969-13 Sequence 13, Appli
41	325.8	66.6	345	2	US-08-794-524-13 Sequence 13, Appli
42	325.8	66.6	345	3	US-09-189-193-13 Sequence 3, Appli
43	45.6	9.3	60	3	US-08-842-947-3 Sequence 11, Appli
44	37.8	7.7	37948	1	US-09-251-645-11 Sequence 42, Appli
45	36.6	7.5	3660	1	US-08-158-232-42

ALIGNMENTS

RESULT 1
: Sequence 4, Application US/08031399
: Patent No. 5552303
: GENERAL INFORMATION:
: APPLICANT: Grabstein, Kenneth
: APPLICANT: Anderson, Dirk
: APPLICANT: Eisenman, June
: APPLICANT: Fung, Victor
: APPLICANT: Rauch, Charles
: TITLE OF INVENTION: Epithelium-derived T-cell factor
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/031,399
: FILING DATE: 19930308
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Launer, Charlene
: REGISTRATION NUMBER: 33,035
: TELEPHONE/DOCKET NUMBER: 2811
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-587-0430
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 489 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..489
: US-08-031-399-4
Query Match 100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e+124; Indels 0; Gaps 0;
Matches 489; Conservative 0; Mismatches 0;

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QY 1 ATGAGAAATTCGAACACATTTGAGAGATTTCCATCCAGTCTACTGTGTTACTT 60
Db 1 ATGAGAAATTCGAACACATTTGAGAGATTTCCATCCAGTCTACTGTGTTACTT 60
QY 61 CTAAACAGTCATTTTCTAACTGAGTGGCATTCATGCTTTCATTTGGGCTGTTTCA 120
Db 61 CTAAACAGTCATTTTCTAACTGAGTGGCATTCATGCTTTCATTTGGGCTGTTTCA 120
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QY 301 GAGTCCGAGATGCAAGTATTCATGATGATGATGATGATGATGATGATGATGAT 360
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QY 361 AGTTGCTTCTTAATGGAATGTACAGAAATCTGATGCAAAAGTGTAGGAATG 420
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QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTCA 480
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QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 2
US-08-393-305-1
; Sequence 1, Application US/08393305
; Patent No. 5574138
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,305
; FILING DATE: 22-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McMaisters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: 1..489
; US-08-393-305-1

Query Match 100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACACATTTGAGAGATTTCCATCCAGTCTACTGTGTTACTT 60
Db 1 ATGAGAAATTCGAACACATTTGAGAGATTTCCATCCAGTCTACTGTGTTACTT 60
QY 61 CTAAACAGTCATTTTCTAACTGAGTGGCATTCATGCTTTCATTTGGGCTGTTTCA 120
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Db 121 GCAGGGCTTCTAAACAGACCACTGGGTGATGTAATAGTGAATTTGAAAAAAT 180
QY 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 3
US-08-535-733-1
; Sequence 1, Application US/08535733
; Patent No. 5660824
; GENERAL INFORMATION:
; APPLICANT: Quinn, Lebris
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Trout, Anthony B.
; TITLE OF INVENTION: Muscle-Trophic Factor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7, Word 5.1a

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,733
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2833
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-08-535-733-1

Query Match 100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTTGGAACCAACATTTAGAGATTTTCATCCAGTCTACTGTGTTACTT 60
DB 1 ATGGAATTTGGAACCAACATTTAGAGATTTTCATCCAGTCTACTGTGTTACTT 60
QY 61 CTTAAACAGTCAATTTCTAAGTGAAGTGGATGATGATGATGATGATGATGATGAT 120
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QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 4
US-08-726-817-1
Sequence 1, Application US/08726817
Patent No. 5707616
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June

APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,817
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-08-726-817-1

Query Match 100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTTGGAACCAACATTTAGAGATTTTCATCCAGTCTACTGTGTTACTT 60
DB 1 ATGGAATTTGGAACCAACATTTAGAGATTTTCATCCAGTCTACTGTGTTACTT 60
QY 61 CTTAAACAGTCAATTTCTAAGTGAAGTGGTGAATGATGATGATGATGATGATGAT 120
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Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGAGATTTCGAACACATTTGAGAGATTTCCATCCAGTGTACTGTGTACTT 60
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DB 481 ACTTCTTGA 489
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RESULT 7

US-08-725-969-1
Sequence 1, Application US/08725969
Patent No. 5892001
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,969
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.

REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-08-725-969-1

Query Match 100.0%; Score 489; DB 2; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 ATGAGATTTCGAACACATTTGAGAGATTTCCATCCAGTGTACTGTGTACTT 60
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DB 1 ATGAGATTTCGAACACATTTGAGAGATTTCCATCCAGTGTACTGTGTACTT 60
OY 61 CTAAACAGTATTTTCTACTGAGTGTGATTTCAATGTTTGGCTGTTCAGT 120
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DB 421 GAAAAAATATTTAAAGATTTTGGCAGATTTGTACATATTTGTCCAAATGTCATCA 480
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DB 481 ACTTCTTGA 489
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RESULT 8

US-08-794-524-1
Sequence 1, Application US/08794524
Patent No. 5985262
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle

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US-09-134-132-2
: Sequence 2, Application US/09134132
: Patent No. 6013480
: GENERAL INFORMATION:
: APPLICANT: Grabstein, Kenneth
: APPLICANT: Paxton, Raymond
: APPLICANT: Pettit, Dean
: TITLE OF INVENTION: Antagonists of IL-15
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: Word for Windows 95, 7.0
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/134,132
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/392,317
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Malaska, Stephen L.
: REGISTRATION NUMBER: 32,655
: REFERENCE/DOCKET NUMBER: 2831
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-587-0430
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 489 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..489
: US-09-134-132-2

Query Match          100.0%; Score 489; DB 3; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.0e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 ATGACATTTTGGAAACCAACATTGGAGAGTATTTCCATCCAGTGCTACTGTGTTACTT 60
Db 1 ATGAGAAATTTGGAAACCAACATTGGAGAGTATTTCCATCCAGTGCTACTGTGTTACTT 60
Y 61 CTAACACATCATTTTCTTACTGCAAGCTGGCATTCATGTCCTTCATTTTGGGCTGTTTCAGT 120
Db 61 CTAACACATCATTTTCTTACTGCAAGCTGGCATTCATGTCCTTCATTTTGGGCTGTTTCAGT 120
Y 121 GCAGGGCTTCTTAAGACAGAACCAACTGGGATGTAAATAAGGATTTTGGAAAAAATT 180
Db 121 GCAGGGCTTCTTAAGACAGAACCAACTGGGATGTAAATAAGGATTTTGGAAAAAATT 180
Y 181 GAAGATCTTATTCATCTATGATCATATTTGATGCTACTTATATATAGGAAAGTATGTTTAC 240
Db 181 GAAGATCTTATTCATCTATGATCATATTTGATGCTACTTATATATAGGAAAGTATGTTTAC 240
Y 241 CCCAGTTGCCAAGTAAGCAAGTAAGAGCTTCTGCTGGAGCTAACAGTATATTTCACTT 300
Db 241 CCCAGTTGCCAAGTAAGCAAGTAAGAGCTTCTGCTGGAGCTAACAGTATATTTCACTT 300

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TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-09-134-456-2

Query Match 100.0%; Score 489; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACAAATTTGAAACACACATTTGAGAAATTTCCATCCACTGCTACTTGTACTT 60
DB 1 ATGACAAATTTGAAACACACATTTGAGAAATTTCCATCCACTGCTACTTGTACTT 60
QY 61 CTAACAGCTTTTCTAAGTAACTGCGATTCATGCTTATTTTGGCTGTTCACT 120
DB 61 CTAACAGCTTTTCTAAGTAACTGCGATTCATGCTTATTTTGGCTGTTCACT 120
QY 121 GCAGGGCTTCTTAACAGAACCAAGCTGGTGAATGTAATAGTATTTGAAAAAAT 180
DB 121 GCAGGGCTTCTTAACAGAACCAAGCTGGTGAATGTAATAGTATTTGAAAAAAT 180
QY 181 GAAGATCTTATTCATATGCAATGTAATGTAATGTAATGTAATGTAATGTAATG 240
DB 181 GAAGATCTTATTCATATGCAATGTAATGTAATGTAATGTAATGTAATGTAATG 240
QY 241 CCCAGTTCAAGATGTAAGCAATGTAATGTAATGTAATGTAATGTAATGTAATG 300
DB 241 CCCAGTTCAAGATGTAAGCAATGTAATGTAATGTAATGTAATGTAATGTAATG 300
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DB 301 GAGTCCGAGATGCAAGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 360
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DB 361 AGTTGCTTTCTAATGGAATGTAACAGATGTAATGTAATGTAATGTAATGTAATG 420
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DB 421 GAAAAAATTTAAAGATTTTTCAGAGTTTGTACATTTGTCCTCAATGTTCAAC 480
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DB 481 ACTTCTTGA 489

RESULT 12
US-09-196-427-2
Sequence 2, Application US/09196427
Patent No. 6177079
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Paxton, Raymond
TITLE OF INVENTION: Antagonists of IL-15
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Word for Windows 95, 7.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,427

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/392,317
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-09-196-427-2

Query Match 100.0%; Score 489; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACAAATTTGAAACACACATTTGAGAAATTTCCATCCACTGCTACTTGTACTT 60
DB 1 ATGACAAATTTGAAACACACATTTGAGAAATTTCCATCCACTGCTACTTGTACTT 60
QY 61 CTAACAGCTTTTCTAAGTAACTGCGATTCATGCTTATTTTGGCTGTTCACT 120
DB 61 CTAACAGCTTTTCTAAGTAACTGCGATTCATGCTTATTTTGGCTGTTCACT 120
QY 121 GCAGGGCTTCTTAACAGAACCAAGCTGGTGAATGTAATAGTATTTGAAAAAAT 180
DB 121 GCAGGGCTTCTTAACAGAACCAAGCTGGTGAATGTAATAGTATTTGAAAAAAT 180
QY 181 GAAGATCTTATTCATATGCAATGTAATGTAATGTAATGTAATGTAATGTAATG 240
DB 181 GAAGATCTTATTCATATGCAATGTAATGTAATGTAATGTAATGTAATGTAATG 240
QY 241 CCCAGTTCAAGATGTAAGCAATGTAATGTAATGTAATGTAATGTAATGTAATG 300
DB 241 CCCAGTTCAAGATGTAAGCAATGTAATGTAATGTAATGTAATGTAATGTAATG 300
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DB 301 GAGTCCGAGATGCAAGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 360
QY 361 AGTTGCTTTCTAATGGAATGTAACAGATGTAATGTAATGTAATGTAATGTAATG 420
DB 361 AGTTGCTTTCTAATGGAATGTAACAGATGTAATGTAATGTAATGTAATGTAATG 420
QY 421 GAAAAAATTTAAAGATTTTTCAGAGTTTGTACATTTGTCCTCAATGTTCAAC 480
DB 421 GAAAAAATTTAAAGATTTTTCAGAGTTTGTACATTTGTCCTCAATGTTCAAC 480
QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 13
US-09-189-193-1
Sequence 1, Application US/09189193
Patent No. 6184359
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June


```

Db      181  GAAGATCTTATTCATCATCATCATATTCATGATGCTACTTTTATATACGGAACATGATTTCCAC 240
Oy      241  CCCAGTTGCCAAAGTATACAGCATATAAGTGGCTTTCTCTTGAGATTACAGTATATTCACCTT 3000
Db      241  CCCAGTTGCCAAAGTATACAGCATATAAGTGGCTTTCTCTTGAGATTACAGTATATTCACCTT 3000
Oy      301  GAGTCCGAGATGCAAGATTCATGATCATAGATACAGATATCTGATCATCTTCATACGAACACAC 3600
Db      301  GAGTCCGAGATGCAAGATTCATGATCATAGATACAGATATCTGATCATCTTCATACGAACACAC 3600
Oy      361  AGTTTGTCTTCTTAATGGGAATGTAAACAGAAATCTGGATGCAAAAGAAATGTGAGAACTGGAG 4200
Db      361  AGTTTGTCTTCTTAATGGGAATGTAAACAGAAATCTGGATGCAAAAGAAATGTGAGAACTGGAG 4200
Oy      421  GAAAAAAATATTTAAAGAAATTTTTCGACAGTTTGTGTACATATATGTCTCAAAATGTTTCATCAC 4800
Db      421  GAAAAAAATATTTAAAGAAATTTTTCGACAGTTTGTGTACATATATGTCTCAAAATGTTTCATCAC 4800
Oy      481  ACTTCTTGA 489
Db      481  ACTTCTTGA 489

RESULT 15
PCT-US96-06423-1
: Sequence 1, Application PC/TUS9606423
: GENERAL INFORMATION:
: APPLICANT: Immunex Corporation
: TITLE OF INVENTION: Muscle Trophic Factor
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: System 7, Word 6.0
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US96/06423
: FILING DATE: 07 May 1996
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Malaska, Stephen L.
: REGISTRATION NUMBER: 32,655
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-587-0430
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 489 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..489
PCT-US96-06423-1

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Query Match	100.0%;	Score 489;	DB 5;	Length 489;
Best Local Similarity	100.0%;	Pred. No. 1.6e-124;		
Matches 489; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy 1 ATGAGAAATTTGGAACCCACATTTGAGAGCATTTCCATCCAGTGTACTTGTGTTACTT 600
|||||
1 ATGAGAAATTTGGAACCCACATTTGAGAGCATTTCCATCCAGTGTACTTGTGTTACTT 600

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Qy	121	GCAGGGCTTCCATAAACGAAAGCCAACTGGGTGAATTAATTAAGTGAATTTGAAAAAAATTT	180
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Dp	181	GAAGATCTTATTCATCATCTATGCAATATTGATGCTACTTTATATACGAAAGTATGTTTCAC	240
Qy	241	CCCAAGTTCGAAAGTAAACGCAATGAAGCTTCTCTTGGAGTTACAAAGTTATTTTCACCT	300
Dp	241	CCCAAGTTCGAAAGTAAACGCAATGAAGCTTCTCTTGGAGTTACAAAGTTATTTTCACCT	300
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Dp	301	GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAAAAATCTGATCATCTAGCAAAACAC	360
Qy	361	AGTTGTCTCTAATGGGAATGTAACGAATCTGGATGCAAAAGATGTGAGAACTGGAG	420
Dp	361	AGTTGTCTCTAATGGGAATGTAACGAATCTGGATGCAAAAGATGTGAGAACTGGAG	420
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Dp	421	GAAAAAAATATTTAAAGAATTTTTCACAGATTTTGTACATATTTGTCCAAAAGTTTCATCAAC	480
Qy	481	ACTTCTTGA 489	
Dp	481	ACTTCTTGA 489	

Search completed: June 19, 2002, 00:51:46
Job time: 4734 sec

Wed Jun 19 09:13:56 2002

us-09-724-841-1.rni

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 00:50:34 ; Search time 2237.54 Seconds
(without alignments)
2949.673 Million cell updates/sec

Title: US-09-724-841-4

Perfect score: 489

Sequence: 1 ATGAGAAATTCGAAACACACA.....TGTTCATCAGACCTCTTGA 489

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

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2: em_esthum:*	2: em_esthum:*
3: em_estlin:*	3: em_estlin:*
4: em_estluc:*	4: em_estluc:*
5: em_estlov:*	5: em_estlov:*
6: em_estpl:*	6: em_estpl:*
7: em_estro:*	7: em_estro:*
8: em_hic:*	8: em_hic:*
9: gb_estl:*	9: gb_estl:*
10: gb_estl2:*	10: gb_estl2:*
11: gb_hic:*	11: gb_hic:*
12: gb_gss:*	12: gb_gss:*
13: em_gss_hum:*	13: em_gss_hum:*
14: em_gss_inv:*	14: em_gss_inv:*
15: em_gss_pln:*	15: em_gss_pln:*
16: em_gss_vrt:*	16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	95.1	982	9	AL548180
2	407.8	87.4	994	9	AL572832
3	377	77.1	509	9	AA463370
4	331.6	67.8	800	10	BG184658
5	276.6	56.6	637	9	AI860008
6	274.4	56.1	756	10	B17832895
7	236	48.3	872	10	B1758668
8	209	42.7	826	10	B1685688
9	165	33.7	690	9	AI596704
10	163.4	33.4	309	10	BF095213
11	161.2	33.0	471	10	N76741
12	151.6	31.0	515	10	BF704348
13	145.4	29.7	538	9	AI152482
14	145	29.7	564	9	AA863763
15	144.8	29.6	474	10	N49734
16	138	28.2	631	9	BB661271
17	126	25.8	166	10	BF379349

18	111.2	22.7	181	9	AA497102	AA497102
19	104.6	21.4	597	9	AA544986	AA544986
20	102.4	20.9	810	10	B1756810	B1756810
21	99.4	20.3	458	9	BB825167	BB825167
22	98.4	20.1	430	9	AA838938	AA838938
23	96.6	19.8	420	10	BE690327	BE690327
24	86.8	17.8	550	10	BE698667	BE698667
25	84.6	17.3	648	9	AA874636	AA874636
26	84.4	17.3	429	9	AA863979	AA863979
27	82.8	16.9	718	10	B1766231	B1766231
28	81.8	16.7	434	9	AI503618	AI503618
29	80.4	16.4	494	9	AA804168	AA804168
30	74	15.1	405	9	AM121368	AM121368
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32	72.2	14.8	275	10	BF088272	BF088272
33	72.2	14.7	483	9	AA804165	AA804165
34	71.2	14.6	509	9	AI120615	AI120615
35	56.6	11.6	987	12	CNS014P0	AL104456
36	54.2	11.1	278	9	BE177883	BE177883
37	52.8	10.8	391	12	AZ334843	AZ334843
38	52.8	9.6	1101	12	CNS000M2	AL063247
39	45.8	9.4	2017	11	BC004164	BC004164
40	45.6	9.3	1101	12	CNS00396	AL063921
41	44.6	9.1	1204	12	CNS016E2	AL106628
42	44	9.0	540	10	B1814723	B1814723
43	44	9.0	584	10	B1815297	B1815297
44	43.2	8.8	740	10	BM167297	BM167297
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ALIGNMENTS

RESULT	1	982 bp	mrna	linear	EST 16-FEB-2001
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LOCUS	AL548180	982 bp	mrna	linear	EST 16-FEB-2001
DEFINITION	AL548180	982 bp	mrna	linear	EST 16-FEB-2001
ACCESSION	AL548180	982 bp	mrna	linear	EST 16-FEB-2001
VERSION	AL548180	982 bp	mrna	linear	EST 16-FEB-2001
KEYWORDS	AL548180	982 bp	mrna	linear	EST 16-FEB-2001
SOURCE	AL548180	982 bp	mrna	linear	EST 16-FEB-2001
ORGANISM	AL548180	982 bp	mrna	linear	EST 16-FEB-2001
REFERENCE	AL548180	982 bp	mrna	linear	EST 16-FEB-2001
AUTHORS	AL548180	982 bp	mrna	linear	EST 16-FEB-2001
TITLE	AL548180	982 bp	mrna	linear	EST 16-FEB-2001
JOURNAL	AL548180	982 bp	mrna	linear	EST 16-FEB-2001
COMMENT	AL548180	982 bp	mrna	linear	EST 16-FEB-2001

FEATURES

FEATURES	source
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/clone_id="LFI_NFL006_PL2"	/clone_id="LFI_NFL006_PL2"
/tissue="placenta"	/tissue="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@life.com URL: http://fulllength.invitrogen.com"	/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive, Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@life.com URL: http://fulllength.invitrogen.com"
BASE COUNT	275 a 208 c 214 g 284 t
ORIGIN	1 others

Query Match 95.1%; Score 465; DB 9; Length 982;
 Best Local Similarity 96.9%; Pred. No. 1.4e-93;
 Matches 474; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACACATTTGAGAGATTTTCATCCAGCTGCTACCTGTTTACTT 60
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 Db CTAAGAGCTATTTCTTACGATGAAGCTGATCATCTTCTTCTTCTTCTTCTTCTTCTT 477
 QY 121 GCAGGCTCCCTAAACAGAGCCCACTGGTGAATGTAATAGTATTGAAAAAAT 180
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 QY 181 GAGATCTTATTCATCTATGATATTTGATGCTACTTATATATACAGAAAGTATGTCAC 240
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 QY 421 GAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTTGTCCAATATGTTCTCAAC 480
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 QY 481 ACTTCTTGA 489
 Db ACTTCTTGA 846

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 VERSION AL572832.1 GI:12931481
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 994)
 AUTHORS L.W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.
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 1..994
 /organism="Homo sapiens"
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 /clone_id="LTI.NFL006.PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; site.1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by
 life Technologies. Contact : Feng Liang life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://Fulllength.invitrogen.com"

BASE COUNT 333 a 186 c 154 g 316 t 5 others
 ORIGIN

Query Match 83.4%; Score 407.8; DB 9; Length 994;
 Best Local Similarity 95.4%; Pred. No. 7.5e-81;
 Matches 415; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

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 Db TTCACTGAGGCTCCCTAAACAGAGCCCACTGGGTAATGTAATAGTATTTGAAA 875
 QY 175 AAAATTGAAGATCTTATTCATCTATGATATTTGATGCTACTTATATACAGAAAGTAT 234
 Db AAAATTGAAGATCTTATTCATCTATGATATTTGATGCTACTTATATACAGAAAGTAT 815
 QY 235 GTTCAACCCAGTTCAGAGTACAGCATGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTT 294
 Db GTTCAACCCAGTTCAGAGTACAGCATGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 755
 QY 295 TCACATGATCCGAGATACAGATATTCATGATACAGTAAATCTTATCATCTTACCA 354
 Db TCACATGATCCGAGATACAGATATTCATGATACAGTAAATCTTATCATCTTACCA 695
 QY 355 AACAAATCTTCTTCTTATATGGAATATACAGATCTGATGCAAAAGTGTGAGAA 414
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 QY 415 CTGAGGAGAAAAATATTAAGATTTTTCAGAGTTTGTACATATTTGTCCAATATGTTCT 474
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RESULT 3
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 DEFINITION similar to SW:IL15_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ;, mRNA
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 VERSION AA463370.1 GI:2188254
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 509)
 AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
 Kuwaba,T., Lacy,M., Le,N., Lennon,G., Merril,M., Martin,J., Moore,B.,
 Schellenberg,K., Steptoe,M., Tan,F., Theisling,B., White,Y., Wyllie,
 T., Waterston,R. and Wilson.R.
 TITLE WashU-Merck EST Project 1997
 JOURNAL Unpublished (1997)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.jnl.gov) for further information. Possible reversed clone: similarity on wrong strand. Seq primer: 28ml3 rev2 ET from Amersham. High quality sequence stop: 416.

FEATURES

source

```

1..509
/organism="Homo sapiens"
/db_xref="GDB:6042614"
/db_xref="taxon:9606"
/clone="IMAGE:811703"
/clone_lib="Soares.NhMPu.S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below). Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI. Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NBHPU, and fetal heart NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
BASE COUNT      149 a      91 c      108 g      161 t
ORIGIN

```

Query Match Best Local Similarity 96.3%; Pred. No. 5.3e-74; Matches 366; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```

QY 1 ATGAGATTTCGAACCACTTTGAGAAGTATTTCCATCCAGTGCCTGTTTACTT 60
   |||||
DB 105 ATGAGATTTCGAACCACTTTGAGAAGTATTTCCATCCAGTGCCTGTTTACTT 164
QY 61 CTAAAGATCATTTTCTAATGTAAGTGCATTCATCTTCAATTTGGGCTGTTTCA 120
   |||||
DB 165 CTAAAGATCATTTTCTAATGTAAGTGCATTCATCTTCAATTTGGGCTGTTTCA 224
QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGTAATAGTGAATTTGAAAAAAT 180
   |||||
DB 225 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGTAATAGTGAATTTGAAAAAAT 284
QY 181 GAAGATCTTATTCATCTATGATGATCTACTTATATACAGAAAGTATGTTTCA 240
   |||||
DB 285 GAAGATCTTATTCATCTATGATGATGATCTACTTATATACAGAAAGTATGTTTCA 344
QY 241 CCCAGTTCAGAGTAAACAGCAATGAGTCTTCTCTGGAATTCAGATTATTTCA 300
   |||||
DB 345 CCCAGTTCAGAGTAAACAGCAATGAGTCTTCTCTGGAATTCAGATTATTTCA 404
QY 301 GAGTCGGAGATACAGATATTCATGATGATGATGATGATGATGATGATGATGAT 360
   |||||
DB 405 GAGTCGGAGATACAGATATTCATGATGATGATGATGATGATGATGATGATGAT 464
QY 361 ATCTTGCTCTTATGGAATATTAACAGAAATCTGATGCAA 401
   |||||
DB 465 AGTTTGCTCTTATGGAATATTAACAGAAATCTGATGCAA 505

```

```

RESULT 4
LOCUS BG184658 800 bp mRNA linear EST 21-Apr-2001
DEFINITION RST3720 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG184658
VERSION BG184658.1 GI:13706473
KEYWORDS EST.
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE

1 (bases 1 to 800)
Harrington J.J., Shert B., Rundlett S., Jackson P.D., Perry R., Cain S., Leventhal C., Thornton M., Ramchandran R., Whittington J., Lerner L., Costanzo D., McElligott K., Booser S., Mays R., Smith E., Veloso N., Kilka A., Hess J., Cottrill K., Lo K., Offenbacher J., Danzig J., and Ducar M.

TITLE

Creation of genome-wide protein expression libraries using random activation of gene expression

JOURNAL

Nat. Biotechnol. 19 (5), 440-445 (2001)

MEDLINE

21227151

COMMENT

Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com

FEATURES

High quality sequence stop: 444.
Location/Qualifiers
1..800

BASE COUNT 235 a 151 c 165 g 247 t

ORIGIN

Query Match Best Local Similarity 67.8%; Score 331.6; DB 10; Length 800; Matches 424; Conservative 0; Mismatches 54; Indels 10; Gaps 5;

```

QY 1 ATGGAATTTTCGAACCACTTTGAGAAGTATTTCCATCCAGTGCCTGTTTACTT 60
   |||||
DB 265 ATGGAATTTTCGAACCACTTTGAGAAGTATTTCCATCCAGTGCCTGTTTACTT 324
QY 61 CTAAAGATCATTTTCTAATGTAAGTGCATTCATCTTCAATTTGGGCTGTTTCA 120
   |||||
DB 325 CTAAAGATCATTTTCTAATGTAAGTGCATTCATCTTCAATTTGGGCTGTTTCA 384
QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGTAATAGTGAATTTGAAAAAAT 180
   |||||
DB 385 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGTAATAGTGAATTTGAAAAAAT 444
QY 181 GAAGATCTTATTCATCTATGATGATGATGATGATGATGATGATGATGATGAT 240
   |||||
DB 445 GAAGATCTTATTCATCTATGATGATGATGATGATGATGATGATGATGATGAT 504
QY 241 CCCAGTTCAGAGTAAACAGCAATGAGTCTTCTCTGGAATTCAGATTATTTCA 300
   |||||
DB 505 CCCAGTTCAGAGTAAACAGCAATGAGTCTTCTCTGGAATTCAGATTATTTCA 564
QY 301 GAGTCGGAGATACAGATATTCATGATGATGATGATGATGATGATGATGATGAT 360
   |||||
DB 565 GAGTCGGAGATACAGATATTCATGATGATGATGATGATGATGATGATGATGAT 622
QY 361 ATCTTGCTCTTATGGAATATTAACAGAAATCTGATGCAA 420
   |||||
DB 623 AT-TTGGCTCTTAATGGG---ATGATACAAATCTGTGCAAGATGAGAGACCTGAG 678
QY 421 GAAAAAATATTAAGATTTTTCAGAGTTTGTATGATATTTGCCAATGTTCAATCA 480
   |||||
DB 679 G-AAAAATTTTAAAGAAATTTTGAAGATTTTGCCCTATTTGG--CAATGTTCTCAAC 734
QY 481 ACTTCTTG 488
   |||||
DB 735 ACTTTTGG 742

```

```

RESULT 5
A1860008 637 bp mRNA linear EST 07-MAR-2000
LOCUS A1860008/c
DEFINITION mm22g03.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2436724 3'
similar to SW:IL15_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ; mRNA
sequence.
ACCESSION A1860008
VERSION A1860008.1 GI:5513624
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 637)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 3944 Std Error: 0.00
Seq primer: -400P from Glibco
High quality sequence stop: 410.
FEATURES
source
location/Qualifiers
1..637
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2436724"
/clone_lib="NCI_CGAP_Ut4"
/tissue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"
BASE COUNT 207 a 111 c 91 g 227 t 1 others
ORIGIN
Query Match 56.6%; Score 276.6; DB 9; Length 637;
Best Local Similarity 95.0%; Pred. No. 1.1e-51;
Matches 285; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 190 ATTCAATTCATGATGATGCTCTTATATACAGAAAGGATGTCACCCAGTTGC 249
|||||
DB 637 ATTCAATTCATGATGATGCTCTTATATACAGAAAGGATGTCACCCAGTTGC 578
QY 250 AAGTACAGCAATGAGTCTTCTCTTGAGTTGCAATGATTCACATGATGCCGA 309
|||||
DB 577 AAGTACAGCAATGAGTCTTCTCTTGAGTTGCAATGATTCACATGATGCCGA 518
QY 310 GATACAGATTCATGATGATGAGTAAATCTTATCATCTAGCAACAACATCTTGTCT 369
|||||
DB 517 GATCAGATTCATGATGATGAGTAAATCTTATCATCTAGCAACAACATCTTGTCT 458
QY 370 TCTATGGAGTATTAAGCATCTGAGTCAAGAAATGTGAGAACTGAGGAAAAAAT 429
|||||
DB 457 TCTATGGAGTATTAAGCATCTGAGTCAAGAAATGTGAGAACTGAGGAAAAAAT 398
QY 430 ATTAAAGATTTTTCAGAGTTTGTATACATTTGTCAAAATGTTTCATCAACTCTTGA 489
|||||
DB 397 ATTAAAGATTTTTCAGAGTTTGTATACATTTGTCAAAATGTTTCATCAACTCTTGA 338

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RESULT 6
B1832895 756 bp mRNA linear EST 04-OCT-2001
LOCUS B1832895
DEFINITION 603082478F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5221771 5',
mRNA sequence.
ACCESSION B1832895
VERSION B1832895.1 GI:15944445
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM11557 row: k column: 20
High quality sequence stop: 756.
FEATURES
source
location/Qualifiers
1..756
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5221771"
/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb; insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH-MGC Library."
BASE COUNT 247 a 115 c 143 g 251 t
ORIGIN
Query Match 56.1%; Score 274.4; DB 10; Length 756;
Best Local Similarity 95.9%; Pred. No. 3.5e-51;
Matches 303; Conservative 0; Mismatches 11; Indels 2; Gaps 2;
QY 174 AAAAATTTGAAGATCTTATTCATCTATGCAATATGATGCTACTTATATACAGAAAGTGA 233
|||||
DB 1 AAAAATTTGAAGATCTTATTCATCTATGCAATATGATGCTACTTATATACAGAAAGTGA 60
QY 234 TGTCAACCCCATGTCGAAGTGAAGCAATGAGCTTCTCTTGAGATTCGCAAGTTAT 293
|||||
DB 61 TGTCAACCCCATGTCGAAGTGAAGCAATGAGCTTCTCTTGAGATTCGCAAGTTAT 120
QY 294 TTTCACATGAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCATCTTAC 353
|||||
DB 121 TTTCACATGAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCATCTTAC 180
QY 354 AAACACATCTTGTCTTCTTAATGGAATTAACAGAAATCGATGCAAGAAATGTGAGGA 413
|||||
DB 181 AAACACACA-GTTGTCTTCTTAATGGAATTAACAGAAATCGATGCAAGAAATGTGAGGA 239
QY 414 ACTAGAGGAAAAAATTAAGAAATTTTTCAGAGTTTGTATACATTTGTCAAAATGTT 473
|||||
DB 240 ACTGAGGAAAAAATTAAGAAATTTTTCAGAGTTTGTATACATTTGTCAAAATGTT 298

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QY 474 CATCAACACTTCTTGA 489
 |||||
 Db 299 CATCAACACTTCTTGA 314

RESULT 7
 BI758686 872 bp mRNA linear EST 25-SEP-2001
 LOCUS 603024240F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5194977 5',
 DEFINITION mRNA sequence.
 ACCESSION BI758686
 VERSION BI758686.1 GI:15750264
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 872)
 NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: L14M11487 row: 0 column: 10
 High quality sequence start: 24
 High quality sequence stop: 859.
 Location/Qualifiers

FEATURES

Source
 1..872
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5194977"
 /clone_1id="NIH_MGC_114"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:
 this is a NIH_MGC Library."
 BASE COUNT 200 a 222 c 227 g 223 t
 ORIGIN

Query Match 48.3%; Score 236; DB 10; Length 872;
 Best Local Similarity 97.1%; Pred. No. 1.2e-42;
 Matches 272; Conservative 0; Mismatches 5; Indels 3; Gaps 3;
 QY 1 ATGAGATTGGAACCACTTTGGAAGTATTTCCATCCAGTGTACTGTTACTT 60
 |||||
 Db 592 ATGAGATTGGAACCACTTTGGAAGTATTTCCATCCAGTGTACTGTTACTT 651
 |||||
 QY 61 CTAAGAGCTATTTCTAAGCACTGGCAATTCATTTGGGCTGTTCACT 120
 |||||
 Db 632 CTAAGAGCTATTTCTAAGCACTGGCAATTCATTTGGGCTGTTCACT 711
 |||||
 QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAATGTAATGATTTGA-AAAAAT 179
 |||||
 Db 712 GCAGGGCTCCCTAAACAGAACCACTGGGTAATGTAATGATTTGA-AAAAAT 771
 |||||
 QY 180 TGAAGATCTTATCAATCTATGCAATTTGATGCTTTATATACAGAAAGTATTCAC 239
 |||||
 Db 772 TGAAGATCTTATCAATCTATGCAATTTGATGCTTTATATACAGAAAGTATTCAC 831
 |||||

QY 240 -CCCCAGTGCAGTAACA-GCAATGAAGTCTTCTCT 277
 |||||
 Db 832 CCCCCAGTGCAGTAACAAGCAATGAAGTCTTCTCT 871
 |||||

RESULT 8
 BI685688 826 bp mRNA linear EST 18-SEP-2001
 LOCUS 603309529F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5345382 5',
 DEFINITION mRNA sequence.
 ACCESSION BI685688
 VERSION BI685688.1 GI:15648316
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Scuriognath; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 826)
 NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: L14M11877 row: j column: 07
 High quality sequence stop: 826.
 Location/Qualifiers

FEATURES

Source
 1..826
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5345382"
 /clone_1id="NCI CGAP Mam6"
 /sex="female, virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-Sport6; Site_1: SalI;
 Site_2: NotI. Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"
 BASE COUNT 212 a 218 c 174 g 222 t
 ORIGIN

Query Match 42.7%; Score 209; DB 10; Length 826;
 Best Local Similarity 79.1%; Pred. No. 1.2e-36;
 Matches 273; Conservative 0; Mismatches 70; Indels 2; Gaps 2;
 QY 1 ATGAGATTGGAACCACTTTGGAAGTATTTCCATCCAGTGTACTGTTACTT 60
 |||||
 Db 481 ATGAGATTGGAACCACTTTGGAAGTATTTCCATCCAGTGTACTGTTACTT 540
 |||||
 QY 61 CTAAGAGCTATTTCTAAGCACTGGCAATTCATTTGGGCTGTTCACT 120
 |||||
 Db 541 CTAAGAGCTATTTCTAAGCACTGGCAATTCATTTGGGCTGTTCACT 599
 |||||
 QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAATGTAATGATTTGA-AAAAAT 180
 |||||
 Db 600 GCAGGGCTCCCTAAACAGAACCACTGGGTAATGTAATGATTTGA-AAAAAT 659
 |||||
 QY 181 GAAGATCTTATCAATCTATGCAATTTGATGCTTTATATACAGAAAGTATTCAC 240
 |||||
 Db 660 GAAGATCTTATCAATCTATGCAATTTGATGCTTTATATACAGAAAGTATTCAC 718
 |||||
 QY 241 CCCAGTGCAGTAACAAGCAATGAAGTCTTCTCTTGGAGTGCAGTTATTCACAT 300
 |||||

[illegible]

QY	309	AGATTACGAAATTCATCATCATACAGTAGAGAAATCTATATCTCTAGCAACAACAATCTTGTG	368
Db	1	AGATGCACGAATTTCATGATGATACAGTAGAGAAATCTGATCTATCTCTACCAACAACAAGTTGGTC	60
QY	369	TTCCTAATGGGAAATATTAACACAGATCTGGATGCTCAAAAGATGTGAGGAACTAGACGAAAAAAA	428
Db	61	TTCCTAATGGGAAATGTATATACAAATCTGGATGCTCAAAAGATGTGAGGAACTGTGAGGAAAAAAA	120

QY	429	TATTAAAGATTTTGGACAGTTTGGTACATATTGGCCAAATGTTCACTTCCTTG	488
Db	121	TATTAAAGATTTTGGACAGTTTGGTACATATTGGCCAAATGTTCACTTCCTTG	180
QY	489	A 489	
Db	181	A 181	
RESULT	11		
LOCUS	N76741		
DEFINITION	N76741	471 bp mRNA linear EST 02-APR-1996	
ACCESSION	Y282912.1	Soares, multiple_sclerosis_2NDHSCP Homo sapiens cDNA	
VERSION	clone IMAGE:889606 5'	similar to SW:IL15_HUMAN P40933	
KEYWORDS	INTEREUKIN-15 PRECURSOR ; mRNA sequence.		
SOURCE	N76741		
ORGANISM	N76741.1	GI:1239319	
	EST.		
	human.		
	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 471)		
	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman		
	, M., Hulman, M., Kucaba, T., Le, M., Lemmon, G., Maitra, M., Parsons, J.,		
	, R., Williamson, A., Soares, M., Tan, F., Trevasakis, E., Waterston		
	The WashU-Merck EST Project		
TITLE	Unpublished (1995)		
JOURNAL	Contact: Wilson RK		
COMMENT	Washington University School of Medicine		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: est@watson.wustl.edu		
	This clone is available royalty-free through LIND; contact the		
	IMAGE Consortium (info@image.lind.gov) for further information.		
	Seq primer: reverse ER		
	High quality sequence stop: 296.		
FEATURES	Location/Qualifiers		
source	1..471		

Query Match	33.0%	Score 161.2;	DB 10;	Length 471;
Best Local Similarity	93.2%;	Pred. No. 5.4e-26;		
Matches 177;	Conservative 0;	Mismatches 12;	Indels 1;	Gaps 1.

QY 301 GAGTCGGAGATACAGATTTCATGATACAGTAGAAGAAATCTTATTCATCTCTACCAACACAC 360

Db	Qy	Db	Qy	Db	Qy	RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT
4	361	124	480	184	421	12	BF704348/c	MI-P-03-aba-f-02-1-UM.s1	BF704348	BF704348	EST.	PIG.	Sus scrofa	1	Bonaldo,M.F., Lennon,G. and Soares,M.B.	Normalization and subtraction: two approaches to facilitate gene	Genome Res. 6 (9), 791-806 (1996)	97044477	Contact: Tugale CK
63	420	183	479	193	479	22-DEC-2000	515 bp	linear	MI-P-03-aba-f-02-1-UM.s1	MI-P-03-aba-f-02-1-UM 3', mRNA sequence.	BF704348	GI:11989750	Euteleostomi;	1	Bonaldo,M.F., Lennon,G. and Soares,M.B.	Normalization and subtraction: two approaches to facilitate gene	Genome Res. 6 (9), 791-806 (1996)	97044477	Contact: Tugale CK

FEATURES	source
Location/Qualifiers	
1..515	
/organism="Sus scrofa"	
/strain="crossbreed"	
/db_xref="taxon:9823"	
/clone="M1-P-03-aba-F-02-1-UM"	
/clone_1fb="M1-P-03"	
/lab_host="DHL0B (Life Technologies)"	
/note="Vector: pRT3b-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The M1-P-03 library is derived from ovary at estrus day 12. For a detailed description of the library from which this clone was derived, please visit our web site at http://bigest.genome.iastate.edu/ ."	
TAG.lib=M1-P-03	
TAG.TISSUE=ovary at estrus day 12	
TAG_SEQ=TTGTGAC	
158 a	91 c 85 g 176 t 5 others

ORIGIN

Query Match 31.0%; Score 151.6; DB 10; Length 515;

Best Local Similarity 84.1%; Pred. No. 7.3e-24;

Matches 169; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 289 GTTATTTTCATGACGAGATACAGATATTCATGATACAGTAAATCTTATCTC 348
 DB 512 GTTCATTTTCAAGAGCTCAGAAATTCAGACATTTAGTATACAGTAAACCTTATCTC 453
 QY 349 CTAGCAACACATCTTCTCTTCTAATGGAATATACAGATCTGATGCAAAAGATCT 408
 DB 452 CTTCGAAACAGAGTTTATGTCATGTAGTATTAACATGATCTGATGCAAAAGATCT 393
 QY 409 GAGCACTAGAGCAAAAAATATTAAGATTTTTCAGAGATTTTTCATATATTTCTCAA 468
 DB 392 GAGGAGCTGAGCAAAAAATATTAAGATTTTTCAGAGATTTTTCATATATTTCTCAA 333
 QY 469 ATGTTTCATCACACTTCTTGA 489
 DB 332 ATGTTTCATCACACTTCTTGA 312

RESULT 13
 A1152482 538 bp mRNA linear EST 30-SEP-1998

LOCUS udb83d09.r1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone

DEFINITION IMAGE:1477457 5' similar to gb:U14332 Mus musculus Interleukin 15

(MOUSE); mRNA sequence.

ACCESSION A1152482 GI:3680951

VERSION EST.

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 538)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

CONTACT: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

MGI:925813

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 326.

Location/Qualifiers

1..538

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone_1ib="Soares_mammary_gland_NMLMG"

/sex="female (lactating)"

/tissue_type="mammary gland"

/lab_host="DH10B"

/note="Vector: pRT73D-pac (Pharmacia) with a modified

polylinker; 1st strand cDNA was prepared from mammary

gland tissue from a lactating female, and was then primed

with a Not I - oligo(dT) primer. Double-stranded cDNA was

ligated to Eco RI adaptors (Pharmacia), digested with Not

I and cloned into the Not I and Eco RI sites of the

modified pRT73 vector. Library is normalized. Library

BASE COUNT 163 a 108 c 103 g 163 t 1 others

was constructed by Bento Soares and M. Fatima Bonaldo.

ORIGIN

Query Match 29.7%; Score 145.4; DB 9; Length 538;

Best Local Similarity 74.9%; Pred. No. 1.7e-22;

Matches 182; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 247 TCGAAGTACAGCAAGAGAGTCTTCTCTTGGAGTTGCAAGTATTTACATGAGTCTC 306
 DB 532 TCGAAGTACTGCAAGAGAGTCTTCTCTTGGAGTTGCAAGTATTTACATGAGTCTC 473
 QY 307 GGAGATACAGATATTCATATACAGTAAATCTTATTCATCTAGCAACACATCTTG 366
 DB 472 AGTAAATGAGTCTTATGAAACAGTAAAGTCTGCTTACCTTGCAGAACAGCAGCTG 413
 QY 367 TCTTCTAATGGGAATATACAGATCTGATGCAAGAAATGTGAGAACTAGAGAAAA 426
 DB 412 TCTTCTAAGAAATGTAGCAGAAATCTGCTGCAAGAAATGTGAGAACTAGAGAAAA 353
 QY 427 AATATTAAGATTTTTCAGAGTTTGTACATATTTGCAAAATGTTTCATCACACTTCT 486
 DB 352 ACCTTCACAGAGTTTTCGAAAGCTTTATACGATTTGCAAAATGTTTCATCACACTTCT 293
 QY 487 TGA 489
 DB 292 TGA 290

RESULT 14

AA863763 564 bp mRNA linear EST 11-MAR-1998

LOCUS vx08d07.r1 Soares_thymus_2NBMt Mus musculus cDNA clone

DEFINITION IMAGE:1263853 5' similar to gb:U14332 Mus musculus Interleukin 15

(MOUSE); mRNA sequence.

ACCESSION AA863763 GI:2956242

VERSION EST.

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 564)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

CONTACT: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

MGI:666405

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 433.

Location/Qualifiers

1..564

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone_1ib="Soares_thymus_2NBMt"

/sex="male"

/tissue_type="thymus"

/dev_stage="4 weeks"

/lab_host="DH108"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
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 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. RNA
 provided by Dr. Bertrand Jordan. Library went through two
 rounds of normalization, and was constructed by Bento
 Soares and M. Fatima Bonaudo."

Query Match	29.7%	Score 145;	DB 9;	length 564;
Best Local Similarity	80.2%	Pred. No. 2,1e-22;		
Matches 194;	Conservative	0;	Mismatches 46;	Indels 2;
			Gaps	2

OY 1 ATGAGATTTTCCAAACCACTTTTGAGAAGTATTTCATCCAGACTACTGTCTACT 60
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 Db 278 ATGAATAATTTGAAACCATAATGTAGAGNAATCAATCCATCTCGTCTACTGTGTTTTCTT 337

[illegible]

D_b

398 GTAGTGCT-CCTAAACAGAGAGCCCACTGGATGATGTAAAGATATGACTGGAGAAGATT 456

[illegible]

Qy	24.1	CC	24.2
Db	516	CC	517

RESULT 15	LOCUS	DEFINITION	ACCESSTION
N49734/C	474 bp	linear	EST 14-FEB-1996
N49734	cyto06b12.s1 Soares_multiple_sclerosis 2NBHMP Homo sapiens	CDNA	
	IMAGE:282239 3' similar to SW-IL15_HUMAN P40933		
	INTERLEUKIN-15 PRECURSOR ;, mRNA sequence.		
	M02734		

VERSION	N49734.1	GI:1190900
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS

Eudaivola, Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 474)
Hillier, L., Clark, N.,
Dubuque, T., Ellison, K.,
Hawkins, M., Holman

TITLE The Washu-Merck Est Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800
Fax: 314 286 1810

This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Seq primer: m13 -40 forward High quality sequence stop: 263.

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FEATURES
source
location/Qualifiers
1..474
/Organism="Homo sapiens"

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/db_xref="taxon:9606"
/clone="IMAGE:282239"
/clone_lib="Soares_multiple_sclerosis_2nbhmsp"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/notice="vector: pUT73D (Pharmacia) with a modified
polylinker V type: phagemid; site_1: Not I; site_2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(OT)
primer 15',
5'GTTACCAATCTGAAGTGGCAGAGCGCCGACATTTTTTTTTTTTTTTT 3',
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pUT73 vector
(Pharmacia). Library run through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis
lesions from one patient was kindly provided by Dr. Kevin
G. Becker (NINDS/NIH).

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Query Match	29.6%	Score 14.4.8:	DB 10;	Length 474;
Best Local Similarity	92.5%	Pred. No. 2.4e-22;		
Matches 149;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0;

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 Db 413 AATCTGATGCANGAATGTCTGAGCACTGGAGAGAAAAAATATTAAAGAATTTTTCGACA 354
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OY	449	GTTTGTGACATATTGGCCAAATGTTCAATCAACTCTTTGA	489
Dδ	353	GTTTGTGACATATTGCCAAATGTTCAATCAACTCTTTGA	313

Search completed: June 19, 2002, 00:50:36
Job time: 6344 sec

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FEATURES
source
location/Qualifiers
1..474
/Organism="Homo sapiens"

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 00:51:46 ; Search time 60.38 Seconds
(without alignments)
1989.314 Million cell updates/sec

Title: US-09-724-841-4

Perfect score: 489
Sequence: 1 ATGAGATTTCGAAACACA.....TCTTCATCAACACTTCTTGA 489

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
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- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	489	100.0	489	1	US-08-031-399-1 Sequence 1, Appl1
2	489	100.0	489	1	US-08-393-305-4 Sequence 4, Appl1
3	489	100.0	489	1	US-08-726-817-4 Sequence 4, Appl1
4	489	100.0	489	1	US-08-504-042-1 Sequence 1, Appl1
5	489	100.0	489	1	US-08-392-317B-1 Sequence 1, Appl1
6	489	100.0	489	2	US-08-725-969-4 Sequence 4, Appl1
7	489	100.0	489	2	US-08-794-524-4 Sequence 4, Appl1
8	489	100.0	489	3	US-09-134-132-1 Sequence 1, Appl1
9	489	100.0	489	4	US-09-134-134A-1 Sequence 1, Appl1
10	489	100.0	489	4	US-09-134-456-1 Sequence 1, Appl1
11	489	100.0	489	4	US-09-196-427-1 Sequence 1, Appl1
12	489	100.0	489	4	US-09-189-193-4 Sequence 1, Appl1
13	489	100.0	489	5	PCT-US94-03793-1 Sequence 1, Appl1
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17	489	100.0	489	1	US-08-335-733-1 Sequence 1, Appl1
18	489	100.0	489	1	US-08-726-817-1 Sequence 1, Appl1
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33	345	70.6	345	1	US-08-393-305-13 Sequence 13, Appl1
34	345	70.6	345	1	US-08-726-817-13 Sequence 13, Appl1
35	345	70.6	345	2	US-08-725-969-13 Sequence 13, Appl1
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39	325.8	66.6	345	1	US-08-726-817-12 Sequence 12, Appl1
40	325.8	66.6	345	2	US-08-725-969-12 Sequence 12, Appl1
41	325.8	66.6	345	2	US-08-794-524-12 Sequence 12, Appl1
42	325.8	66.6	345	4	US-09-189-193-12 Sequence 12, Appl1
43	45.6	9.3	60	3	US-08-842-947-3 Sequence 3, Appl1
44	36.6	7.5	3660	1	US-08-158-232-42 Sequence 42, Appl1
45	36.6	7.5	3660	1	US-08-611-928-42 Sequence 42, Appl1

ALIGNMENTS

RESULT 1
US-08-031-399-1
Sequence 1, Application US/08031399
Patent No. 5552303
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: Epithelium-derived T-cell Factor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,399
FILING DATE: 19930308
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Launer, Charlene
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-08-031-399-1
Query Match 100.0%; Score 489; DB 1; Length 489;

Best Local Similarity 100.0%; Pred. No. 1.6e-123; Indels 0; Gaps 0;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 2
US-08-393-305-4
; Sequence 4, Application US/08393305
; Patent No. 5574138
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,305
; FILING DATE: 22-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
; US-08-393-305-4

Query Match 100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-123; Indels 0; Gaps 0;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACACATTTGAGAAATTTCCATTCAGTCTGTTACTT 60
DB 1 ATGAGATTTCGAACACACATTTGAGAAATTTCCATTCAGTCTGTTACTT 60
QY 61 CTAAGAGATCTTTCTAATCTGAGTCTGATTCATGCTTATTTGGGCTGTTCACT 120
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QY 181 GAAGATCTTATTCATCTATGCAATTTGATGCTTATTAATACAGAAAGTATGTTCAAC 240
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QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 3
US-08-726-817-4
; Sequence 4, Application US/08726817
; Patent No. 5707616
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,817
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052,409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-08-726-817-4

Query Match 100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-123;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACACATTTGAGAATATTCATCCAGTCGCTGTTTACTT 60
DB 1 ATGAGAAATTCGAACACATTTGAGAATATTCATCCAGTCGCTGTTTACTT 60
QY 61 CTAAAGAGTCATTTTCTAACTGAAGCTGCATTCATCTTCAATTTGGGCTGTTTCACT 120
DB 61 CTAAAGAGTCATTTTCTAACTGAAGCTGCATTCATCTTCAATTTGGGCTGTTTCACT 120
QY 121 GCAGGGCTCCCTAAACAGAACCAACTGGGTAATGTAATAGTATTTGAAAAAATT 180
DB 121 GCAGGGCTCCCTAAACAGAACCAACTGGGTAATGTAATAGTATTTGAAAAAATT 180
QY 181 GAAGATCTATTCATCTATGATATGATGCTACTTTATATACAAAGTGTTTCAC 240
DB 181 GAAGATCTATTCATCTATGATATGATGCTACTTTATATACAAAGTGTTTCAC 240
QY 241 CCCAGTTGCAAGGTAAACAGCAATGAAGTCTTCTTGGAGTTGCAAGTTATTTACAT 300
DB 241 CCCAGTTGCAAGGTAAACAGCAATGAAGTCTTCTTGGAGTTGCAAGTTATTTACAT 300
QY 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTATATCTCTAGCAAAACAC 360
DB 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTATATCTCTAGCAAAACAC 360
QY 361 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTATATCTCTAGCAAAACAC 360
DB 361 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTATATCTCTAGCAAAACAC 360
QY 421 GAAAAAATATTAAGAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480
DB 421 GAAAAAATATTAAGAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 4
US-08-504-042-1

Sequence 1, Application US/08504042
Patent No. 5747024
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Elsenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: Epithelium-derived T-cell Factor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,042
FILING DATE: 19-JUL-1995
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/031,399
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Launer, Charlene
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-08-504-042-1

Query Match 100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-123;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACACATTTGAGAATATTCATCCAGTCGCTGTTTACTT 60
DB 1 ATGAGAAATTCGAACACATTTGAGAATATTCATCCAGTCGCTGTTTACTT 60
QY 61 CTAAAGAGTCATTTTCTAACTGAAGCTGCATTCATCTTCAATTTGGGCTGTTTCACT 120
DB 61 CTAAAGAGTCATTTTCTAACTGAAGCTGCATTCATCTTCAATTTGGGCTGTTTCACT 120
QY 121 GCAGGGCTCCCTAAACAGAACCAACTGGGTAATGTAATAGTATTTGAAAAAATT 180
DB 121 GCAGGGCTCCCTAAACAGAACCAACTGGGTAATGTAATAGTATTTGAAAAAATT 180
QY 181 GAAGATCTATTCATCTATGATATGATGCTACTTTATATACAAAGTGTTTCAC 240
DB 181 GAAGATCTATTCATCTATGATATGATGCTACTTTATATACAAAGTGTTTCAC 240
QY 241 CCCAGTTGCAAGGTAAACAGCAATGAAGTCTTCTTGGAGTTGCAAGTTATTTACAT 300
DB 241 CCCAGTTGCAAGGTAAACAGCAATGAAGTCTTCTTGGAGTTGCAAGTTATTTACAT 300

QY 301 GAGTCGCGAGATACAGATATTCATGATACAGTACAGAAATCTTATCATCTTACGAAACAC 360
|||||
Db 301 GAGTCGCGAGATACAGATATTCATGATACAGTACAGAAATCTTATCATCTTACGAAACAC 360
QY 361 ATCTTGCTCTTAATGGGAATATACAGAAATCTGATGCAAGAATGTGAGAACTAGAG 420
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Db 361 ATCTTGCTCTTAATGGGAATATACAGAAATCTGATGCAAGAATGTGAGAACTAGAG 420
QY 421 GAAAAAATATTAAGAATTTTTCAGAGATTTGTACATATTTGCCAAATGTTTCATCAAC 480
|||||
Db 421 GAAAAAATATTAAGAATTTTTCAGAGATTTGTACATATTTGCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
|||||
Db 481 ACTTCTTGA 489

RESULT 5

US-08-392-317B-1
; Sequence 1, Application US/08392317B
; Patent No. 5795966
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,317B
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..342
; US-08-392-317B-1

Query Match 100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 1,6e-123;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATTTGGAACCACTTTGGAGATATTTCCATCCAGTGTACTGTTACTT 60
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Db 1 ATGAGAATTTGGAACCACTTTGGAGATATTTCCATCCAGTGTACTGTTACTT 60

QY 61 CTAAGAGTCATTTTCTAAGTGAAGCTGGCAATTCATGCTTTCATTTTGGGCTGTTCACT 120
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Db 61 CTAAGAGTCATTTTCTAAGTGAAGCTGGCAATTCATGCTTTCATTTTGGGCTGTTCACT 120
QY 121 GCAGGGCTCCCTAAACAGAACCCCACTGGGTGAATGTAATTAAGTATTTGAAAAAATT 180
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Db 121 GCAGGGCTCCCTAAACAGAACCCCACTGGGTGAATGTAATTAAGTATTTGAAAAAATT 180
QY 181 GAAGATCTTATTCATATGATGATATGATGCTACTTATATNAGAAAGATGTTCAAC 240
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Db 181 GAAGATCTTATTCATATGATGATATGATGCTACTTATATNAGAAAGATGTTCAAC 240
QY 241 CCCAGTTGCAAGTATACAGCAATGAAGTCTTCTCTTGAGTTGCAAGTATTTTCACAT 300
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Db 241 CCCAGTTGCAAGTATACAGCAATGAAGTCTTCTCTTGAGTTGCAAGTATTTTCACAT 300
QY 301 GAGTCGCGAGATACAGATATTCATGATACAGTACAGAAATCTTATCATCTTACGAAACAC 360
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Db 301 GAGTCGCGAGATACAGATATTCATGATACAGTACAGAAATCTTATCATCTTACGAAACAC 360
QY 361 ATCTTGCTCTTAATGGGAATATACAGAAATCTGATGCAAGAATGTGAGAACTAGAG 420
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Db 361 ATCTTGCTCTTAATGGGAATATACAGAAATCTGATGCAAGAATGTGAGAACTAGAG 420
QY 421 GAAAAAATATTAAGAATTTTTCAGAGATTTGTACATATTTGCCAAATGTTTCATCAAC 480
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Db 421 GAAAAAATATTAAGAATTTTTCAGAGATTTGTACATATTTGCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
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Db 481 ACTTCTTGA 489

RESULT 5

US-08-725-969-4
; Sequence 4, Application US/08725969
; Patent No. 5892001
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,969
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs

TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-08-725-969-4

Query Match 100.0%; Score 489; DB 2; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-123;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGAACACCACTTTGAGAGTATTTCCATCCAGTGTCTGTTACTT 60
DB 1 ATGAGATTTTGAACACCACTTTGAGAGTATTTCCATCCAGTGTCTGTTACTT 60
QY 61 CTAAGAGTCAATTTCTACTGAGCTGGCATTCATGCTTCTCATTTTGGCTGTTCACT 120
DB 61 CTAAGAGTCAATTTCTACTGAGCTGGCATTCATGCTTCTCATTTTGGCTGTTCACT 120
QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGATTAAGTATTGAAAAAATT 180
DB 121 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGATTAAGTATTGAAAAAATT 180
QY 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 CCCAGTTGCAAGGTAAACAGCAATGAGTCTTCTCTGGAGTTGCAAGTTATTTACAT 300
DB 241 CCCAGTTGCAAGGTAAACAGCAATGAGTCTTCTCTGGAGTTGCAAGTTATTTACAT 300
QY 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCATCTGCAAAACAC 360
DB 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCATCTGCAAAACAC 360
QY 361 ATCTGTCTTATGGAATATACAGATCTGATGCAAAAGTGTGAGAACTAGAG 420
DB 361 ATCTGTCTTATGGAATATACAGATCTGATGCAAAAGTGTGAGAACTAGAG 420
QY 421 GAAAAAATATTTAAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTCATCAAC 480
DB 421 GAAAAAATATTTAAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTCATCAAC 480
QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 7
US-08-794-524-4
Sequence 4, Application US/08794524
Patent No. 5985262
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,524
FILING DATE: 03-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-08-794-524-4

Query Match 100.0%; Score 489; DB 2; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-123;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGAACACCACTTTGAGAGTATTTCCATCCAGTGTCTGTTACTT 60
DB 1 ATGAGATTTTGAACACCACTTTGAGAGTATTTCCATCCAGTGTCTGTTACTT 60
QY 61 CTAAGAGTCAATTTCTACTGAGCTGGCATTCATGCTTCTCATTTTGGCTGTTCACT 120
DB 61 CTAAGAGTCAATTTCTACTGAGCTGGCATTCATGCTTCTCATTTTGGCTGTTCACT 120
QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGATTAAGTATTGAAAAAATT 180
DB 121 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGATTAAGTATTGAAAAAATT 180
QY 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 CCCAGTTGCAAGGTAAACAGCAATGAGTCTTCTCTGGAGTTGCAAGTTATTTACAT 300
DB 241 CCCAGTTGCAAGGTAAACAGCAATGAGTCTTCTCTGGAGTTGCAAGTTATTTACAT 300
QY 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCATCTGCAAAACAC 360
DB 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCATCTGCAAAACAC 360
QY 361 ATCTGTCTTATGGAATATACAGATCTGATGCAAAAGTGTGAGAACTAGAG 420
DB 361 ATCTGTCTTATGGAATATACAGATCTGATGCAAAAGTGTGAGAACTAGAG 420
QY 421 GAAAAAATATTTAAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTCATCAAC 480
DB 421 GAAAAAATATTTAAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTCATCAAC 480
QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 8
US-09-134-132-1
Sequence 1, Application US/09134132
Patent No. 6013480
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth

APPLICANT: Paxton, Raymond
APPLICANT: Pettit, Dean
TITLE OF INVENTION: Antagonists of IL-15
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Word for Windows 95, 7.0
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,132
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/392,317
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2831
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..342
US-09-134-132-1

Query Match 100.0%; Score 489; DB 3; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-123;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTTGCAACACACATTTGAGAAATATTTCCATCCAGTGCATCTGTTACTT 60
DB 1 ATGAGAAATTTGCAACACACATTTGAGAAATATTTCCATCCAGTGCATCTGTTACTT 60
QY 61 CTTAAGAGTCATTTTCTAATCTGAGAGCTGCATTCATGCTTCAATTTTGGGCTGTTCACT 120
DB 61 CTTAAGAGTCATTTTCTAATCTGAGAGCTGCATTCATGCTTCAATTTTGGGCTGTTCACT 120
QY 121 GGAGGGCTCCCTAAACACAAAGCAAGCTGGTGAATGTAAAGTATTTGAAAAAAT 180
DB 121 GGAGGGCTCCCTAAACACAAAGCAAGCTGGTGAATGTAAAGTATTTGAAAAAAT 180
QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACAGAAAGTGATTTTAC 240
DB 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACAGAAAGTGATTTTAC 240
QY 241 CCCAGTTGCAAGGTAAACAGCAATGAAGTCTTTCTCTGAGTTGCAAGTTATTTTCAAT 300
DB 241 CCCAGTTGCAAGGTAAACAGCAATGAAGTCTTTCTCTGAGTTGCAAGTTATTTTCAAT 300
QY 301 GAGTCCGGAGATACAGATTTTCATGATACAGTAAAGAAATCTTATCTAGCAAAACAC 360
DB 301 GAGTCCGGAGATACAGATTTTCATGATACAGTAAAGAAATCTTATCTAGCAAAACAC 360
QY 361 ACTTGTCTTCTAATGGAATATACAGAAATCTGATGCAAGAAATGTAGAACTAGAG 420

|||||
DB 361 ACTTGTCTTCTAATGGAATATACAGAAATCTGATGCAAGAAATGTAGAACTAGAG 420
QY 421 GAAAAAATATTAAAGATTTTTCGAGAGTTTGTACATATTTGCCAATGTTCATCAAC 480
DB 421 GAAAAAATATTAAAGATTTTTCGAGAGTTTGTACATATTTGCCAATGTTCATCAAC 480
QY 481 ACTTGTCTGA 489
DB 481 ACTTGTCTGA 489

RESULT 9
US-09-134-134A-1
Sequence 1, Application US/09134134A
Patent No. 6165466
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Paxton, Raymond
APPLICANT: Pettit, Dean
TITLE OF INVENTION: Antagonists of IL-15
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Word for Windows 95, 7.0
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,134A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/392,317
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2831
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..342
US-09-134-134A-1

Query Match 100.0%; Score 489; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-123;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTTGCAACACACATTTGAGAAATATTTCCATCCAGTGCATCTGTTACTT 60
DB 1 ATGAGAAATTTGCAACACACATTTGAGAAATATTTCCATCCAGTGCATCTGTTACTT 60
QY 61 CTTAAGAGTCATTTTCTAATCTGAGAGCTGCATTCATGCTTCAATTTTGGGCTGTTCACT 120
DB 61 CTTAAGAGTCATTTTCTAATCTGAGAGCTGCATTCATGCTTCAATTTTGGGCTGTTCACT 120

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; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..342
; US-09-134-456-1

Query Match 100.0%; Score 489; DB 4; Length 489;
Best Local Similarity 100.0%; Prid. No. 1.ee-123;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTGGAACCCACATTGGGAAGTATTTCCATCCAGTGTCTACTGTGTTACT 60
    |||
Db 1 ATGAGATTGGAACCCACATTGGGAAGTATTTCCATCCAGTGTCTACTGTGTTACT 60

QY 61 CTAAGACTCATTTCTTACGTGAGCTGGCATTCAATGCTCATTTTGGCGTGTTCAC 120
    |||
Db 61 CTAAGACTCATTTCTTACGTGAGCTGGCATTCAATGCTCATTTTGGCGTGTTCAC 120

QY 121 GCAGGCTCCCTTAACAGAAAGCCAACTGGGTGAATGTATTAAGTATTGAAAAAATT 180
    |||
Db 121 GCAGGCTCCCTTAACAGAAAGCCAACTGGGTGAATGTATTAAGTATTGAAAAAATT 180

QY 181 GAAGATCTTATTCATCTATGCAATATGTACTTATATACAGAAAGTATGTTCCAC 240
    |||
Db 181 GAAGATCTTATTCATCTATGCAATATGTACTTATATACAGAAAGTATGTTCCAC 240

QY 241 CCCAGTGCAGAGTAACAGCAATGAAGTCTTTCCTTGGAGTGTGCAATATTTCACAT 300
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CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/392,317
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Malaska, Stephen L.
 REGISTRATION NUMBER: 32,655
 REFERENCE/DOCKET NUMBER: 2831
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-587-0430
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 489 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..342
 US-09-196-427-1

Query Match 100.0%; Score 489; DB 4; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.6e-123;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGAACCCACATTTTGAGAGTATTTCCATCCAGTCTGCTGTTACTT 60
 DB 1 ATGAGATTTTGAACCCACATTTTGAGAGTATTTCCATCCAGTCTGCTGTTACTT 60
 QY 61 CTAAGAGTCAATTTTCTAAGTCAAGTGGCATTCATGCTTCTTATTTGGGCTGTTCACT 120
 DB 61 CTAAGAGTCAATTTTCTAAGTCAAGTGGCATTCATGCTTCTTATTTGGGCTGTTCACT 120
 QY 121 GCAGGGCTCCCTAAACAGAACCCAACTGGGTGAATGTAAATGATTGAAAAAATT 180
 DB 121 GCAGGGCTCCCTAAACAGAACCCAACTGGGTGAATGTAAATGATTGAAAAAATT 180
 QY 181 GAAGATCTTATTCATATGATATGATATGATGCTACTTTATATACAGAAAGTATGTCAC 240
 DB 181 GAAGATCTTATTCATATGATATGATATGATGCTACTTTATATACAGAAAGTATGTCAC 240
 QY 241 CCCAGTTCAGAGTAACAGCAATGAAGTCTTCTCTGGAGTTGCAAGTTATTTCCACT 300
 DB 241 CCCAGTTCAGAGTAACAGCAATGAAGTCTTCTCTGGAGTTGCAAGTTATTTCCACT 300
 QY 301 GAGTCGGAGATACAGATATTCATGATACAGTAGAAAAATCTTATCATCTCAGCAAAACAC 360
 DB 301 GAGTCGGAGATACAGATATTCATGATACAGTAGAAAAATCTTATCATCTCAGCAAAACAC 360
 QY 361 ATCTTGCTTCTAATGGAATATATACAGAAATCTGATGCAAAAGATGTGAGAACTAGAG 420
 DB 361 ATCTTGCTTCTAATGGAATATATACAGAAATCTGATGCAAAAGATGTGAGAACTAGAG 420
 QY 421 GAAAAAATATTTAAGATTTTTCAGAGTTTGTACATATATGTCCTCAATGTTTCATCAAC 480
 DB 421 GAAAAAATATTTAAGATTTTTCAGAGTTTGTACATATATGTCCTCAATGTTTCATCAAC 480
 QY 481 ACTTCTTGA 489
 DB 481 ACTTCTTGA 489

RESULT 12
 US-09-189-193-4
 Sequence 4, Application US/09189193
 Patent No. 6184359
 GENERAL INFORMATION:
 APPLICANT: Grabstein, Kenneth
 APPLICANT: Anderson, Dlfk

APPLICANT: Eisenman, June
 APPLICANT: Fung, Victor
 APPLICANT: Rauch, Charles
 TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed and Berry
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/189,193
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/393,305
 FILING DATE: 22-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Mcmasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 480052.409C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-622-4900
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 489 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..489
 US-09-189-193-4

Query Match 100.0%; Score 489; DB 4; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.6e-123;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGAACCCACATTTTGAGAGTATTTCCATCCAGTCTGCTGTTACTT 60
 DB 1 ATGAGATTTTGAACCCACATTTTGAGAGTATTTCCATCCAGTCTGCTGTTACTT 60
 QY 61 CTAAGAGTCAATTTTCTAAGTCAAGTGGCATTCATGCTTCTTATTTGGGCTGTTCACT 120
 DB 61 CTAAGAGTCAATTTTCTAAGTCAAGTGGCATTCATGCTTCTTATTTGGGCTGTTCACT 120
 QY 121 GCAGGGCTCCCTAAACAGAACCCAACTGGGTGAATGTAAATGATTGAAAAAATT 180
 DB 121 GCAGGGCTCCCTAAACAGAACCCAACTGGGTGAATGTAAATGATTGAAAAAATT 180
 QY 181 GAAGATCTTATTCATATGATATGATATGATGCTACTTTATATACAGAAAGTATGTCAC 240
 DB 181 GAAGATCTTATTCATATGATATGATATGATGCTACTTTATATACAGAAAGTATGTCAC 240
 QY 241 CCCAGTTCAGAGTAACAGCAATGAAGTCTTCTCTGGAGTTGCAAGTTATTTCCACT 300
 DB 241 CCCAGTTCAGAGTAACAGCAATGAAGTCTTCTCTGGAGTTGCAAGTTATTTCCACT 300
 QY 301 GAGTCGGAGATACAGATATTCATGATACAGTAGAAAAATCTTATCATCTCAGCAAAACAC 360
 DB 301 GAGTCGGAGATACAGATATTCATGATACAGTAGAAAAATCTTATCATCTCAGCAAAACAC 360
 QY 361 ATCTTGCTTCTAATGGAATATATACAGAAATCTGATGCAAAAGATGTGAGAACTAGAG 420
 DB 361 ATCTTGCTTCTAATGGAATATATACAGAAATCTGATGCAAAAGATGTGAGAACTAGAG 420

Query Match 95.1%; Score 465; DB 1; Length 489;
 Best Local Similarity 96.9%; Pred. No. 4.8e-117;
 Matches 474; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGGAATTTGAAACCACTTTGAGATATTTCCATCCAGTGTCTACTTACTT 60
 DB 1 ATGGAATTTGAAACCACTTTGAGATATTTCCATCCAGTGTCTACTTACTT 60
 QY 61 CTAAGAGTCTATTTCTTAAGTGAAGTGCATTTCTTCAATTTGGGCTGTTTCACT 120
 DB 61 CTAAGAGTCTATTTCTTAAGTGAAGTGCATTTCTTCAATTTGGGCTGTTTCACT 120
 QY 121 GCAGGGCTCCCTAAACCAAGAACCACTGGGTGAATGTAATAGTATTTGAAAAAATT 180
 DB 121 GCAGGGCTCCCTAAACCAAGAACCACTGGGTGAATGTAATAGTATTTGAAAAAATT 180
 QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTATTTACGAAGATGATTTTAC 240
 DB 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTATTTACGAAGATGATTTTAC 240
 QY 241 CCCAGTTGCAAGTACAGCAATGAGTCTTCTCTGAGTTGCAAGTATTTACAT 300
 DB 241 CCCAGTTGCAAGTACAGCAATGAGTCTTCTCTGAGTTGCAAGTATTTACAT 300
 QY 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCTATCTAGCAAAAC 360
 DB 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCTATCTAGCAAAAC 360
 QY 361 ATCTGTCTTTTAATGGAATATTAACAGATCTGATGCAAGATGAGAGACTAAG 420
 DB 361 ATCTGTCTTTTAATGGAATATTAACAGATCTGATGCAAGATGAGAGACTAAG 420
 QY 421 GAAAAAATATTTAAAGATTTTTCAGAGTTTGTACATTTGTCCAATGTTTCATCAAC 480
 DB 421 GAAAAAATATTTAAAGATTTTTCAGAGTTTGTACATTTGTCCAATGTTTCATCAAC 480
 QY 481 ACTTCTTGA 489
 DB 481 ACTTCTTGA 489

RESULT 15
 US-08-393-305-1
 : Sequence 1, Application US/08393305
 : Patent No. 5574138
 : GENERAL INFORMATION:
 : APPLICANT: Grabstein, Kenneth
 : APPLICANT: Anderson, Dirk
 : APPLICANT: Eisenman, June
 : APPLICANT: Fung, Victor
 : APPLICANT: Rauch, Charles
 : TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
 : NUMBER OF SEQUENCES: 15
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Seed and Berry
 : STREET: 6300 Columbia Center, 701 Fifth Avenue
 : CITY: Seattle
 : STATE: Washington
 : COUNTRY: USA
 : ZIP: 98104
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/393,305
 : FILING DATE: 22-FEB-1995
 : CLASSIFICATION: 424
 : ATTORNEY/AGENT INFORMATION:
 : NAME: McMaisters, David D.
 : REGISTRATION NUMBER: 33,963
 : REFERENCE/DOCKET NUMBER: 480052,409C2

TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 206-622-4900
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 489 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 1..489
 : US-08-393-305-1

Query Match 95.1%; Score 465; DB 1; Length 489;
 Best Local Similarity 96.9%; Pred. No. 4.8e-117;
 Matches 474; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGGAATTTGAAACCACTTTGAGATATTTCCATCCAGTGTCTACTTACTT 60
 DB 1 ATGGAATTTGAAACCACTTTGAGATATTTCCATCCAGTGTCTACTTACTT 60
 QY 61 CTAAGAGTCTATTTCTTAAGTGAAGTGCATTTCTTCAATTTGGGCTGTTTCACT 120
 DB 61 CTAAGAGTCTATTTCTTAAGTGAAGTGCATTTCTTCAATTTGGGCTGTTTCACT 120
 QY 121 GCAGGGCTCCCTAAACCAAGAACCACTGGGTGAATGTAATAGTATTTGAAAAAATT 180
 DB 121 GCAGGGCTCCCTAAACCAAGAACCACTGGGTGAATGTAATAGTATTTGAAAAAATT 180
 QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTATTTACGAAGATGATTTTAC 240
 DB 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTATTTACGAAGATGATTTTAC 240
 QY 241 CCCAGTTGCAAGTACAGCAATGAGTCTTCTCTGAGTTGCAAGTATTTACAT 300
 DB 241 CCCAGTTGCAAGTACAGCAATGAGTCTTCTCTGAGTTGCAAGTATTTACAT 300
 QY 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCTATCTAGCAAAAC 360
 DB 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCTATCTAGCAAAAC 360
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 DB 361 ATCTGTCTTTTAATGGAATATTAACAGATCTGATGCAAGATGAGAGACTAAG 420
 QY 421 GAAAAAATATTTAAAGATTTTTCAGAGTTTGTACATTTGTCCAATGTTTCATCAAC 480
 DB 421 GAAAAAATATTTAAAGATTTTTCAGAGTTTGTACATTTGTCCAATGTTTCATCAAC 480
 QY 481 ACTTCTTGA 489
 DB 481 ACTTCTTGA 489

Search completed: June 19, 2002, 00:51:47
 Job time: 4735 sec

Wed Jun 19 09:14:03 2002

us-09-724-841-4.rni

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 00:56:22 ; Search time 1924.67 Seconds
(without alignments)
195.710 Million cell updates/sec

Title: US-09-724-841-9

Sequence: 18
1 AAYTGGCTNAAGTNAATH 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenBank: 1: gb_da: 2: gb_htg: 3: gb_in: 4: gb_om: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vl: 15: em_ba: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_om: 21: em_or: 22: em_ov: 23: em_pat: 24: em_ph: 25: em_pl: 26: em_ro: 27: em_sts: 28: em_un: 29: em_vl: 30: em_htg_hum: 31: em_htg_inv: 32: em_htg_other: 33: em_htgo_inv:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
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1	14.4	80.0	18	6	AR004271	Sequence
2	14.4	80.0	18	6	AR070285	Sequence
3	14.4	80.0	18	6	AR085744	Sequence
4	14.4	80.0	18	6	I25786	Sequence 9
5	14.4	80.0	18	6	I28853	Sequence 9
6	14.4	80.0	18	6	I79223	Sequence 9
7	14.4	80.0	25	6	AR094646	Sequence
8	14.4	80.0	25	6	AR094646	Sequence
9	14.4	80.0	25	6	BD008808	Antagonist
10	14.4	80.0	39	6	AR024354	Sequence
11	14.4	80.0	39	6	AR122051	Sequence
12	14.4	80.0	39	6	AR122873	Sequence
13	14.4	80.0	39	6	AR125110	Sequence
14	14.4	80.0	69	6	AR024356	Sequence
15	14.4	80.0	69	6	AR122053	Sequence
16	14.4	80.0	69	6	AR122875	Sequence
17	14.4	80.0	69	6	AR125112	Sequence
18	14.4	80.0	345	6	AR070288	Sequence
19	14.4	80.0	345	6	AR070289	Sequence
20	14.4	80.0	345	6	AR085747	Sequence
21	14.4	80.0	345	6	AR085748	Sequence
22	14.4	80.0	345	6	I28856	Sequence 12
23	14.4	80.0	345	6	I28857	Sequence 12
24	14.4	80.0	345	6	I79226	Sequence 12
25	14.4	80.0	345	6	I79227	Sequence 13
26	14.4	80.0	380	11	G23879	human STRs
27	14.4	80.0	453	9	HS1L15MR	238000 H. sapiens
28	14.4	80.0	484	5	AB067626	AB067626 Dmidloch
29	14.4	80.0	486	6	HS1L15	Y09908 H. sapiens m
30	14.4	80.0	489	6	AR004267	Sequence
31	14.4	80.0	489	6	AR004268	Sequence
32	14.4	80.0	489	6	AR024348	Sequence
33	14.4	80.0	489	6	AR024349	Sequence
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35	14.4	80.0	489	6	AR070282	Sequence
36	14.4	80.0	489	6	AR085740	Sequence
37	14.4	80.0	489	6	AR085741	Sequence
38	14.4	80.0	489	6	AR094649	Sequence
39	14.4	80.0	489	6	AR094650	Sequence
40	14.4	80.0	489	6	AR122045	Sequence
41	14.4	80.0	489	6	AR122046	Sequence
42	14.4	80.0	489	6	AR122867	Sequence
43	14.4	80.0	489	6	AR122868	Sequence
44	14.4	80.0	489	6	AR125104	Sequence
45	14.4	80.0	489	6	AR125105	Sequence

ALIGNMENTS

RESULT 1	AR004271	18 bp	DNA	1 linear	PAT 04-DEC-1998
LOCUS	AR004271	18 bp	DNA	1 linear	PAT 04-DEC-1998
DEFINITION	Sequence 9 from patent US 5747024.				
ACCESSION	AR004271				
VERSION	AR004271.1	GI:3965150			
KEYWORDS	UNKNOWN.				
SOURCE	UNKNOWN.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 18)				
AUTHORS	Grabstein, K.H. and Widmer, M.B.				
TITLE	Vaccine adjuvant comprising interleukin-15				
JOURNAL	Patent: US 5747024-A 9 05-MAY-1998;				
FEATURES	location/Qualifiers				
source	1..18				
BASE COUNT	5 a 5 c 4 g 4 t 5 others				
ORIGIN	1..18				
Query Match	80.0%; Score 14.4; DB 6; Length 18;				
Best Local Similarity	100.0%; Pred. No. 3.3e+02;				

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGGGTNAAYGTNATH 18
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Db 1 AAYTGGGTNAAYGTNATH 18

RESULT 2
AR070285
LOCUS AR070285 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 9 from patent US 5892001.
ACCESSION AR070285
VERSION AR070285.1 GI:7221173
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 18)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Epithelium-derived T-cell factor antipodles
JOURNAL Patent: US 5892001-A 9 06-APR-1999;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 5 a 0 c 4 g 4 t 5 others
ORIGIN

Query Match 80.0%; Score 14.4; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGGGTNAAYGTNATH 18
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Db 1 AAYTGGGTNAAYGTNATH 18

RESULT 3
AR085744
LOCUS AR085744 18 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 9 from patent US 5985262.
ACCESSION AR085744
VERSION AR085744.1 GI:10012510
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 18)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Method of treatment with epithelium derived T-cell factor
JOURNAL Patent: US 5985262-A 9 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 5 a 0 c 4 g 4 t 5 others
ORIGIN

Query Match 80.0%; Score 14.4; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGGGTNAAYGTNATH 18
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Db 1 AAYTGGGTNAAYGTNATH 18

RESULT 4
I25786
LOCUS I25786 18 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 9 from patent US 5552303.
ACCESSION I25786
VERSION I25786.1 GI:1605656

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 18)
AUTHORS Grabstein,K., Anderson,D., Eisenman,J., Fung,V. and Rauch,C.
TITLE DNA encoding epithelium-derived T-cell factor
JOURNAL Patent: US 5552303-A 9 03-SEP-1996;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 5 a 0 c 4 g 4 t 5 others
ORIGIN

Query Match 80.0%; Score 14.4; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGGGTNAAYGTNATH 18
|||||

Db 1 AAYTGGGTNAAYGTNATH 18

RESULT 5
I28853
LOCUS I28853 18 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 9 from patent US 5574138.
ACCESSION I28853
VERSION I28853.1 GI:1819635
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 18)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Epithelium-derived T-cell factor
JOURNAL Patent: US 5574138-A 9 12-NOV-1996;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 5 a 0 c 4 g 4 t 5 others
ORIGIN

Query Match 80.0%; Score 14.4; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGGGTNAAYGTNATH 18
|||||

Db 1 AAYTGGGTNAAYGTNATH 18

RESULT 6
I79223
LOCUS I79223 18 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 9 from patent US 5707616.
ACCESSION I79223
VERSION I79223.1 GI:3207513
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 18)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Method for treating or preventing gastrointestinal disease with
epithelium-derived T-cell factor
JOURNAL Patent: US 5707616-A 9 13-JAN-1998;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 5 a 0 c 4 g 4 t 5 others

ORIGIN

Query Match

Best Local Similarity 80.0%; Score 14.4; DB 6; Length 18;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18
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DB 1 AAYTGGTNAAYGTNATH 18

RESULT 7

AR094646

LOCUS AR094646 25 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 1 from patent US 6001973.
ACCESSION AR094646
VERSION AR094646.1 GI:10021757
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Strom,T.B. and Maslinski,W.
TITLE Antagonists of Interleukin-15
JOURNAL Patent: US 6001973-A 1 14-DEC-1999;
FEATURES
source 1..25 Location/Qualifiers
/organism="unknown"

BASE COUNT 9 a 2 c 7 g 7 t
ORIGIN

Query Match 80.0%; Score 14.4; DB 6; Length 25;
Best Local Similarity 72.2%; Pred. No. 3.4e+02;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18
|||||
DB 8 AACTGGGTGAATGTATATA 25

RESULT 8
AX320246
LOCUS AX320246 25 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 5 from Patent WO0187330.
ACCESSION AX320246
VERSION AX320246.1 GI:11901654
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (sites)
AUTHORS Strom,T.B. and Maslinski,W.
TITLE Compositions and methods for achieving immune suppression
JOURNAL Patent: WO 0187330-A 5 22-NOV-2001;
FEATURES
source 1..25 Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetically generated oligonucleotide"

BASE COUNT 9 a 2 c 7 g 7 t
ORIGIN

Query Match 80.0%; Score 14.4; DB 6; Length 25;
Best Local Similarity 72.2%; Pred. No. 3.4e+02;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18
|||||
DB 8 AACTGGGTGAATGTATATA 25

RESULT 9

BD008808

LOCUS BD008808 25 bp DNA linear PAT 31-JAN-2002
DEFINITION Antagonists of Interleukin-15.
ACCESSION BD008808
VERSION BD008808.1 GI:18637181
KEYWORDS JP 2001502521-A/1.
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 25)
AUTHORS Strom,T. and Maslinski,W.
TITLE Antagonists of Interleukin-15
JOURNAL Patent: JP 2001502521-A 1 27-FEB-2001;
COMMENT BETH ISRAEL DEACONESS MEDICAL CENTER
OS Unidentified
PN JP 2001502521-A/1
PD 27-FEB-2001
PF 25-APR-1997 JP 1997539046
PR 26-APR-1996 US 60/016634
PI TERRY STROM,MLODZIMERZ MASLINSKI
PC C12N15/24,C07K14/54,A61K38/20,C12N15/62,G01N33/68 CC
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT source 1..25 Location/Qualifiers
/organism="unidentified".
/organism="unidentified"

FEATURES
source 1..25 Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 9 a 2 c 7 g 7 t
ORIGIN

Query Match 80.0%; Score 14.4; DB 6; Length 25;
Best Local Similarity 72.2%; Pred. No. 3.4e+02;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18
|||||
DB 8 AACTGGGTGAATGTATATA 25

RESULT 10
AR024354
LOCUS AR024354 39 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 7 from patent US 5795966.
ACCESSION AR024354
VERSION AR024354.1 GI:3977648
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 39)
AUTHORS Grabsstein,K.H., Pettit,D.K. and Paxton,R.J.
TITLE Antagonists of Interleukin-15
JOURNAL Patent: US 5795966-A 7 18-AUG-1998;
FEATURES
source 1..39 Location/Qualifiers
/organism="unknown"

BASE COUNT 12 a 8 c 9 g 10 t
ORIGIN

Query Match 80.0%; Score 14.4; DB 6; Length 39;
Best Local Similarity 72.2%; Pred. No. 3.5e+02;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18
|||||

Db 22 AACTGGGTGAATGTATA 39

RESULT 11

LOCUS AR122051 39 bp DNA Linear PAT 16-MAY-2001

DEFINITION Sequence 7 from patent US 6165466.

ACCESSION AR122051

VERSION AR122051.1 GI:14106368

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 39)

AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.

TITLE Antagonists of Interleukin-15

JOURNAL Patent: US 6165466-A 7 26-DEC-2000;

FEATURES Location/Qualifiers

source 1..39

BASE COUNT 12 a 8 c 9 g 10 t

ORIGIN

Query Match 80.0%; Score 14.4; DB 6; Length 39;

Best Local Similarity 72.2%; Pred. No. 3.5e+02;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGGTNAAYGTNATH 18

Db 22 AACTGGGTGAATGTATA 39

RESULT 12

LOCUS AR122873 39 bp DNA Linear PAT 16-MAY-2001

DEFINITION Sequence 7 from patent US 6168783.

ACCESSION AR122873

VERSION AR122873.1 GI:14107839

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 39)

AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.

TITLE Antagonists of Interleukin-15

JOURNAL Patent: US 6168783-A 7 02-JAN-2001;

FEATURES Location/Qualifiers

source 1..39

BASE COUNT 12 a 8 c 9 g 10 t

ORIGIN

Query Match 80.0%; Score 14.4; DB 6; Length 39;

Best Local Similarity 72.2%; Pred. No. 3.5e+02;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGGTNAAYGTNATH 18

Db 22 AACTGGGTGAATGTATA 39

RESULT 13

LOCUS AR125110 39 bp DNA Linear PAT 16-MAY-2001

DEFINITION Sequence 7 from patent US 6177079.

ACCESSION AR125110

VERSION AR125110.1 GI:14111172

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 39)

AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.

TITLE Antagonists of Interleukin-15

JOURNAL Patent: US 6177079-A 7 23-JAN-2001;

FEATURES Location/Qualifiers

source 1..39

BASE COUNT 12 a 8 c 9 g 10 t

ORIGIN

Query Match 80.0%; Score 14.4; DB 6; Length 39;

Best Local Similarity 72.2%; Pred. No. 3.5e+02;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGGTNAAYGTNATH 18

Db 22 AACTGGGTGAATGTATA 39

RESULT 14

LOCUS AR024356 69 bp DNA Linear PAT 05-DEC-1998

DEFINITION Sequence 9 from patent US 5795966.

ACCESSION AR024356

VERSION AR024356.1 GI:3977650

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 69)

AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.

TITLE Antagonists of Interleukin-15

JOURNAL Patent: US 5795966-A 9 18-AUG-1998;

FEATURES Location/Qualifiers

source 1..69

BASE COUNT 28 a 8 c 18 g 15 t

ORIGIN

Query Match 80.0%; Score 14.4; DB 6; Length 69;

Best Local Similarity 72.2%; Pred. No. 3.6e+02;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGGTNAAYGTNATH 18

Db 49 AACTGGGTGAATGTATA 66

RESULT 15

LOCUS AR122053 69 bp DNA Linear PAT 16-MAY-2001

DEFINITION Sequence 9 from patent US 6165466.

ACCESSION AR122053

VERSION AR122053.1 GI:14106370

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 69)

AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.

TITLE Antagonists of Interleukin-15

JOURNAL Patent: US 6165466-A 9 26-DEC-2000;

FEATURES Location/Qualifiers

source 1..69

BASE COUNT 28 a 8 c 18 g 15 t

ORIGIN

Query Match 80.0%; Score 14.4; DB 6; Length 69;

Best Local Similarity 72.2%; Pred. No. 3.6e+02;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Oy 1 AAYTGGGTNAAYGTNATH 18
||:||||| |:| |:
Db 49 AACTGGGTGAATGTAATA 66

Search completed: June 19, 2002, 02:54:31
Job time: 7089 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 00:50:42 ; Search time 291.55 seconds
(without alignments)
106.001 Million cell updates/sec

Title: US-09-724-841-9
Perfect score: 18
Sequence: 1 AAYTGCGTNAAYGTNATH 18

Scoring table: IDENTITY_NDC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
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23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	14.4	80.0	18	AA00528	Degenerate PCR pri
2	14.4	80.0	18	AA084585	Simian IL-15 prime
3	14.4	80.0	18	AA049457	Epithelium derived
4	14.4	80.0	18	AA042244	Simian ERF gene pr
5	14.4	80.0	18	AAV02875	Simian epithelium
6	14.4	80.0	18	AA029483	Simian ERF DNA amp
7	14.4	80.0	18	AA038246	Simian ERF degener
8	14.4	80.0	22	AA057021	Simian ERF cDNA sp
9	14.4	80.0	25	AA097224	Mature Interleukin

10	14.4	80.0	39	AA036636	Interleukin-15 PCR
11	14.4	80.0	345	AA000525	Simian Interleukin
12	14.4	80.0	345	AA000527	Human Interleukin
13	14.4	80.0	345	AA057024	Simian ERF (SEF)
14	14.4	80.0	345	AA057025	Human ERF (SEF) m
15	14.4	80.0	466	AA021344	Human low adenosis
16	14.4	80.0	466	AA035222	Human adenosis re
17	14.4	80.0	466	AA00524	Simian Interleukin
18	14.4	80.0	466	AA00526	Human Interleukin
19	14.4	80.0	466	AA084583	Simian IL-15 clone
20	14.4	80.0	466	AA084584	Human IL-15 clone
21	14.4	80.0	466	AA049455	Simian epithelium
22	14.4	80.0	466	AA049456	Human epithelium d
23	14.4	80.0	466	AA042242	Simian epithelium
24	14.4	80.0	466	AA042243	Human epithelium-d
25	14.4	80.0	466	AA036634	Simian Interleukin
26	14.4	80.0	466	AA036635	Human Interleukin
27	14.4	80.0	466	AA097227	Wild-type Interleu
28	14.4	80.0	466	AA097228	Mutant Interleuk
29	14.4	80.0	466	AA058404	Interleukin-15 cod
30	14.4	80.0	466	AA023554	Human Interleukin
31	14.4	80.0	466	AA02874	Human Interleukin
32	14.4	80.0	466	AA02873	Simian epithelium
33	14.4	80.0	466	AA029479	Simian epithelium
34	14.4	80.0	466	AA029480	Human epithelium-d
35	14.4	80.0	466	AA090031	Simian Interleukin
36	14.4	80.0	466	AA090032	Human Interleukin
37	14.4	80.0	466	AA090033	Human Interleukin
38	14.4	80.0	466	AA038244	Simian epithelium
39	14.4	80.0	466	AA038245	Human epithelium-d
40	14.4	80.0	466	AA057017	Human Interleukin
41	14.4	80.0	466	AA057018	Simian ERF (SEF)
42	14.4	80.0	466	AA035436	Human ERF (hERF) p
43	14.4	80.0	790	AA033078	Human colon cancer
44	14.4	80.0	1202	AA056368	Human IL-15 DNA.
45	14.4	80.0	1202	AA021342	Human low adenosis

ALIGNMENTS

RESULT 1	
AA00528	
ID	AA00528 standard; cDNA; 18 BP.
XX	
XX	AA00528:
XX	
DT	02-FEB-1996 (first entry)
XX	
DE	Degenerate PCR primer based on simian IL-15 mature N-terminus.
XX	
KW	Interleukin-15; epithelium-derived T-cell factor; T lymphocyte;
KW	PCR primer; ss.
XX	
OS	Synthetic.
XX	
FH	Key
FT	misc-feature
FT	Location/Qualifiers
FT	1..18
FT	/*tag= a
FT	/note= "std IUPAC codes used"
PN	
PD	W09527722-A.
XX	
XX	19-OCT-1995.
XX	
XX	06-APR-1994; 94WO-US03793.
XX	
XX	06-APR-1994; 94WO-US03793.
XX	
PA	(IMV) IMMUNEX CORP.
XX	
XX	Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI	Rauch C;

XX WPI: 1995-373556/48.
 DR Isolated DNA encoding polypeptide with mammalian IL-15 activity - which
 XX stimulates proliferation and differentiation of T cells, used for
 PT treating carcinoma(s), melanomas, etc. and viral infections
 PT
 XX Example 3: Page 21; 48pp; English.
 PS
 XX A simian species of IL-15 (sIL-15) was purified and analysed by SDS-
 CC PAGE. Bioassay of unstained gel slices indicated IL-15 activity was
 CC assoc. with proteins having mol. wts in the range of 15-17 kDa. The
 CC N-terminus of the 15-17 kDa was sequenced. The results indicated the
 CC identity of the first 33 AAs of AAR83309. Subsequent sequencing of a
 CC cDNA clone obt'd. from a simian library provided a sequence encoding
 CC the polypeptide AAR83436. AAR83436 comprises a relatively short 48 AA
 CC leader sequence and a mature polypeptide AAR83309. The sequence of the
 CC N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers
 CC for the amplification of IL-15-specific DNA sequences. The first
 CC 6 AAs of the N-terminus were used to design one primer, a
 CC degenerate mixture coding for all possible codon usages - AAT00528.
 CC The AA sequences of the simian mature N-terminus 26-31 were used
 CC to design a second primer, a degenerate mixture coding for a
 CC complement of all possible codon usages of AAs 26-31, omitting
 CC postn. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA
 CC cells were used as templates. A 92 bp DNA fragment was used as a
 CC hybridisation probe to screen a portion of a plasmid library contg.
 CC cDNA inserts prep'd. from CV-1/EBNA polyadenylated RNA. This
 CC resulted in the isolation of clone C85.sIL-15 that has an ORF
 CC given in AAT00524. AAR83309 is the active polypeptide & AAR83436 is
 CC the precursor polypeptide.
 SQ Sequence 18 BP; 5 A; 0 C; 4 G; 4 T; 5 other;

Query Match 80.0%; Score 14.4; DB 16; Length 18;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAYTGGGTNAAYGTNATH 18
 ||||||||||||||||
 Db 1 aaytgggtnaaygtath 18

RESULT 2
 AA084585
 ID AA084585 standard; cDNA; 18 BP.
 AC AA084585;
 XX
 DT 04-SEP-1995 (first entry)
 XX
 DE Simian IL-15 primer.
 XX
 KW Interleukin-15; IL-15; sIL-15; T-cell growth factor;
 KM African green monkey; CV-1; antitumor; virucide; primer; PCR;
 KM polymerase chain reaction; ss.
 XX
 OS Synthetic.
 OS
 PN ZA9402636-A.
 XX
 PD 28-DEC-1994.
 XX
 PF 18-APR-1994; 94ZA-0002636.
 XX
 PR 18-APR-1994; 94ZA-0002636.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 PI Rauch C;
 XX

DR WPI: 1995-082473/11.
 XX
 PT New purified interleukin-15 - which induces T cell proliferation
 PT and differentiation, used for the treatment of tumours and viral
 PT infection
 PT
 XX Example 3: Page 21; 47pp; English.
 PS
 XX cDNA generated from PMA-stimulated CV-1/EBNA cells was amplified
 CC by PCR using primers (AA084585-87) based on the N-terminal sequence
 CC of simian interleukin-15 (sIL-15). A clone encoding sIL-15 was
 CC obtained (AA084583).
 CC
 SQ Sequence 18 BP; 5 A; 0 C; 4 G; 4 T; 5 other;

Query Match 80.0%; Score 14.4; DB 16; Length 18;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAYTGGGTNAAYGTNATH 18
 ||||||||||||||||
 Db 1 aaytgggtnaaygtath 18

RESULT 3
 AAT49457
 ID AAT49457 standard; cDNA; 18 BP.
 AC AAT49457;
 XX
 DT 11-MAR-1997 (first entry)
 XX
 DE Epithelium derived T cell factor PCR primer.
 XX
 KW Simian epithelium derived T cell factor; sETF; African green monkey;
 KM Cercopithecus aethiops; CV1/EBNA cell; T-cell; B-cell; lymphocyte;
 KM proliferation; differentiation; gastrointestinal; HIV infection;
 KM human immunodeficiency virus; polymerase chain reaction; ss.
 XX
 OS Synthetic.
 OS
 PN US5574138-A.
 XX
 PD 12-NOV-1996.
 XX
 PF 08-MAR-1993; 93US-0031399.
 XX
 PR 22-FEB-1995; 95US-0393305.
 PR 08-MAR-1993; 93US-0031399.
 PR 22-APR-1994; 94US-0233606.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 PI Rauch C;
 XX
 DR WPI: 1996-517923/51.
 XX
 PT New epithelium derived T cell factor - induces proliferation of T
 PT and B cells, stimulates destruction of tumour and virus-infected
 PT cells and protects against toxicity, partic. for treating intestinal
 PT disease and HIV infection
 PT
 XX Example 3; Column 25; 35pp; English.
 PS
 XX The simian ETF (epithelium derived T cell factor) was isolated from
 CC African green monkey CV1/EBNA cell conditioned medium. The N-
 CC terminal sequence of the purified ETF was determined and then PCR
 CC primers were designed based on the sequence information. The
 CC present sequence is that of a degenerate primer based on the first 6
 CC amino acids, i.e. Asn-Trp-Val-Asn-Val-Ile. A 92 bp fragment was
 CC amplified from CV1/EBNA DNA and was used as a probe to screen a

CC CV1/EBNA CDNA library for the full-length SEF coding sequence.
CC Mature SEF induces proliferation and/or differentiation of precursor
CC or mature T cells and is useful for promoting long-term in vitro
CC culture of T-lymphocytes and T-cell lines. It is used for treating
CC gastrointestinal diseases including peptic ulcer, colitis and
CC malignancy and for treating HIV infection.
XX
SQ Sequence 18 BP; 5 A; 0 C; 4 G; 4 T; 5 other;

Query Match 80.0%; Score 14.4; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAYTGGGTNAAYGTNATH 18
Db 1 aaytg99gnaaygnath 18
|||||

RESULT 4
ID AAT42244 standard; DNA; 18 BP.
AC AAT42244;
XX
DT 05-FEB-1997 (first entry)
XX
DE Simian ERF gene primer based on the 6 N-terminal amino acids.
XX
KW Epithelium-derived T-cell factor; simian; human; culture; proliferation;
KW epithelial cell; differentiation; T-lymphocyte; African green monkey;
KW primer; PCR; polymerase chain reaction; amplification; probe; ss.
OS Synthetic.
XX
PN USS552303-A.
PD 03-SEP-1996.
XX
PF 08-MAR-1993; 93US-0031399.
XX
PR 08-MAR-1993; 93US-0031399.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;
XX
DR WPI: 1996-412063/41.
XX
PT New isolated simian and human epithelium-derived T-cell factors -
PT which stimulate the proliferation and/or differentiation of
PT T-lymphocytes and T-cell lines
XX
PS Example 3; Column 17; 22pp; English.
XX
CC Primers AAT42244-6 were used to amplify a 92 bp fragment of the African
CC green monkey epithelium-derived T-cell factor (ERF; AAT42243). The
CC sequence of this primer is based on the 6 N-terminal amino acids sequence
CC obtained by peptide sequencing the purified protein. The template for
CC the amplification was cDNA derived from monkey kidney CV-1/EBNA cells
CC stimulated to proliferate by phorbol 12-myristate 13-acetate. The 92 bp
CC fragment was labelled and used as a probe to isolate a clone C85. SEF
CC which contained the simian gene. ERF is a protein of 15-17 kD which is
CC expressed by epithelial cells and stimulates proliferation and/or
CC differentiation of precursor and/or mature T cells. The protein is
CC therefore useful for promoting long term in vivo culture of
CC T-lymphocytes and T-cell lines.
XX
SQ Sequence 18 BP; 5 A; 0 C; 4 G; 4 T; 5 other;

Query Match 80.0%; Score 14.4; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 91;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAYTGGGTNAAYGTNATH 18
Db 1 aaytg99gnaaygnath 18
|||||

RESULT 5
ID AAV02875 standard; DNA; 18 BP.
XX
AC AAV02875;
XX
DT 08-MAY-1998 (first entry)
XX
DE Simian epithelium derived T-cell factor PCR primer 1.
XX
KW Epithelium derived T-cell factor; ERF; simian; gastrointestinal disease;
KW B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;
KW treatment; prevention; PCR primer; ss.
OS Synthetic.
XX
PN USS707616-A.
PD 13-JAN-1998.
XX
PF 04-OCT-1996; 96US-0726817.
XX
PR 22-FEB-1995; 95US-0393305.
PR 08-MAR-1993; 93US-0031399.
PR 22-APR-1994; 94US-0233606.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI Rauch C;
XX
DR WPI: 1998-100295/09.
XX
PT Treatment or prevention of gastrointestinal diseases - by
PT administering epithelium-derived T-cell factor polypeptide
XX
PS Example 3; Column 41-42; 34pp; English.
XX
CC PCR primers AAV02875-V02877 are used in the amplification of a simian
CC epithelium-derived T-cell factor (ERF) which is used in a method for
CC treating or preventing gastrointestinal disease. These polypeptides have
CC particular application in the treatment of gastrointestinal disorders
CC associated with disruption of the gastrointestinal epithelium or villi
CC such as chemotherapy- and radiation-therapy induced enteritis (gut
CC toxicity), mucositis, peptic ulcer disease, gastroenteritis and colitis,
CC villus atrophic disorders, malignancy and inflammatory bowel disease.
CC ERF polypeptides may also be useful in the treatment of human
CC immunodeficiency virus (HIV) and HIV-associated disease due to their
CC ability to stimulate CD4+ and CD8+ cells. Biologically active ERF may be
CC used to treat a variety of other diseases or conditions where T-cell or
CC B-cell stimulation is desired.
XX
SQ Sequence 18 BP; 5 A; 0 C; 4 G; 4 T; 5 other;

Query Match 80.0%; Score 14.4; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAYTGGGTNAAYGTNATH 18
Db 1 aaytg99gnaaygnath 18
|||||

RESULT 6

AAZ29483
ID AAZ29483 standard: DNA: 18 BP.
XX
AC AAZ29483;
XX
DT 10-JUN-1999 (first entry)
XX
DE Simlan ETF DNA amplifying primer.
XX
KW Epithelium-derived T-cell factor; ETF; immunoassay; enteritis; ulcer;
KW T cell proliferation; gastrointestinal disease; mucositis; colitis;
KW gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease;
KW human immune deficiency virus; tumour; simlan; PCR primer; ss.
XX
OS Synthetic.
OS
PN US5892001-A.
XX
PD 06-APR-1999.
XX
PF 04-OCT-1996; 96US-0725969.
XX
PR 22-FEB-1995; 95US-0393305.
PR 08-MAR-1993; 93US-0031399.
PR 22-APR-1994; 94US-0233606.
PR 04-OCT-1996; 96US-0725969.
XX
PA (IMNV) IMMUNEX CORP.
XX
PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI Rauch C;
XX
DR WPI: 1999-253930/21.
XX
PT Antibodies specific for epithelium-derived T-cell growth factor
XX
PS Example 3: Columns 25; 34pp: English.
XX
CC The invention relates to an isolated antibody that binds specifically to
CC a simlan or human epithelium-derived T-cell factor (ETF) polypeptide.
CC The antibodies are used, optionally when immobilized or labeled, to
CC detect and quantify ETF in standard immunoassays. They may also be used
CC as diagnostic and therapeutic agents, e.g. when conjugated to toxins (or
CC their precursors) or radionuclides. ETF induces proliferation and/or
CC differentiation of T cells (or their precursors), e.g. for use in
CC establishing long term in vitro cultures; and is also used to treat
CC gastrointestinal disease (e.g. enteritis or mucositis induced by
CC chemotherapy or radiation, peptic ulcer, gastroenteritis, colitis,
CC villus atrophy, malignancy and inflammatory bowel disease), to treat
CC human immune deficiency virus infection or associated disease, or
CC generally in any situation requiring stimulation of T or B cell
CC proliferation, secretion of immunoglobulins or certain cytokines.
CC increased anti-infectious disease immunity, induction of T-cell lytic
CC activity or increased destruction of tumour or virus-infected cells.
CC Sequences AAZ29483-85 represent primers for PCR amplification of the
CC simlan ETF DNA sequences.
XX
SQ Sequence 18 BP; 5 A; 0 C; 4 G; 4 T; 5 other;

Query Match 80.0%; Score 14.4; DB 20; length 18;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGGCTNAAYGCTNATH 18
|||
Db 1 aaytggctnaaygctnath 18

RESULT 7
AAZ38246
ID AAZ38246 standard: DNA: 18 BP.
XX

AAZ38246;
AC
XX
DT 09-FEB-2000 (first entry)
XX
DE Simlan ETF degenerate PCR primer #9.
XX
KW ETF; epithelium-derived T-cell factor; T-cell; T-lymphocyte;
KW proliferation; differentiation; growth factor; precursor; mature; CD4+;
KW CD8+; gastrointestinal; epithelium; cell culture; treatment; HIV;
KW gastrointestinal disease; gastroenteritis; colitis;
KW inflammatory bowel disease; villus atrophic disorder; enteritis;
KW chemotherapy; radiotherapy; gut toxicity; cancer; side effect;
KW tolerated dose; PCR; primer; ss.
XX
OS Synthetic.
OS
PN Mammalia.
XX
PD US5985262-A.
XX
PF 16-NOV-1999.
XX
PR 03-FEB-1997; 97US-0794524.
XX
PR 22-FEB-1995; 95US-0393305.
PR 04-OCT-1996; 96US-0726817.
PR 08-MAR-1993; 93US-0031399.
PR 22-APR-1994; 94US-0233606.
XX
PA (IMNV) IMMUNEX CORP.
XX
PI Rauch C, Fung V, Eisenman JR, Grabstein KH, Anderson DM;
PI P-PSDB: AAZ52312.
XX
DR WPI: 2000-022267/02.
XX
PT Stimulation of T-cells in human immunodeficiency virus infected
XX
PS patients -
XX
CC Example 3: Column 25; 33pp: English.
XX
CC This sequence represents simlan ETF degenerate PCR primer #9, used with
CC degenerate primers #10 or #11 (AAZ38247, AAZ38248) to amplify a fragment
CC of the gene encoding simlan epithelium-derived T-cell factor (ETF).
CC This was used to probe a simlan cDNA library for a clone with a
CC complete open reading frame (AAZ38224). The primers were based on
CC N-terminal amino acid sequences in the purified ETF protein.
CC ETF is a previously unidentified T-cell growth factor which
CC stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to
CC proliferate and differentiate. It also promotes proliferation of the
CC gastrointestinal epithelium. The protein can be used to promote long-term
CC in vitro culture of T-lymphocytes and T-cell lines. ETF can be used for
CC treating HIV infection. HIV-associated diseases, and other diseases or
CC conditions where stimulation of T-cell proliferation would be desirable
CC e.g., it could be used to augment the destruction of tumour cells or
CC virally infected cells. ETF may also be used to treat or prevent
CC gastrointestinal disease, including chemotherapy and radiotherapy
CC associated enteritis, gastroenteritis, colitis, inflammatory bowel
CC disease and villus atrophic disorders. Chemotherapy and radiotherapy
CC associated enteritis (gut toxicity) results in bleeding and sepsis due to
CC gastrointestinal flora entering the blood, and thus can limit the dosage
CC of therapeutic agent administered to a cancer patient. ETF may therefore
CC be used to increase the tolerated doses radiotherapy and chemotherapy.
XX
SQ Sequence 18 BP; 5 A; 0 C; 4 G; 4 T; 5 other;

Query Match 80.0%; Score 14.4; DB 21; length 18;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGGCTNAAYGCTNATH 18
|||
Db 1 aaytggctnaaygctnath 18

[illegible]

DT 17-NOV-1996 (first entry)
 XX Interleukin-15 PCR primer NTFIL15B.
 DE Interleukin-15 PCR primer NTFIL15B.
 XX Interleukin-15; antagonist; mutein; graft versus host disease;
 KW allograft; T-cell growth factor; polymerase chain reaction;
 KW PCR; primer; ss.
 XX Synthetic.
 OS
 XX WO9626274-A1.
 PM
 XX 29-AUG-1996.
 PD
 XX 21-FEB-1996; 96MO-US02520.
 PF
 XX 22-FEB-1995; 95US-0392317.
 PR
 XX (IMMV) IMMUNEX CORP.
 PA
 XX Grabstein KH, Paxton RJ, Pettit DK;
 PI
 XX WPI: 1996-402367/40.
 DR
 XX Antagonists of Interleukin-15 - are used to treat patients having
 PT symptoms of graft-versus-host disease and for prolonging allo-graft
 survival
 PT
 XX Example 1; Page 17; 32pp; English.
 PS
 XX PCR primers NTFIL15B (AAT36636) and NTFIL15F (AAT36637) are used
 CC for the primary amplification of simian or human interleukin-15
 CC DNA sequences (see also AAT36634-35), when maintenance of the
 CC mature sequences is desired. A secondary amplification uses
 CC primers that incorporate restriction sites into the amplified
 CC sequence to allow incorporation of the product into yeast
 CC expression vector palpaADH2. Other primers used for primary
 CC PCR produce sequences coding for IL-15 muteins having amino acid
 CC substitutions at positions D56 and/or Q156. Such muteins are
 CC antagonists of IL-15 and can be used to treat graft-versus-host
 CC disease and to prolong allograft survival.
 CC
 XX Sequence 39 BP; 12 A; 8 C; 9 G; 10 T; 0 other;
 SQ

Query Match 80.0%; Score 14.4; DB 17; Length 39;
 Best Local Similarity 72.2%; Pred. No. 99;
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGGCTNAAYGTNATH 18
 ||:||||| ||:| ||:
 Db 22 aactgggtgaatgtaata 39

RESULT 11
 AAT00525
 ID AAT00525 standard; cDNA: 345 BP.
 XX
 AC AAT00525;
 XX
 DT 02-FEB-1996 (first entry)
 XX
 DE Simian interleukin-15 mature polypeptide.
 XX
 KW Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.
 XX
 OS Cebus apella.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..345
 FT /*tag- a
 FT /label= precursor nts 145-489
 FT /note= "claimed"

XX
 PN WO952722-A.
 PD
 XX 19-OCT-1995.
 PD
 XX 06-APR-1994; 94MO-US03793.
 PF
 XX 06-APR-1994; 94MO-US03793.
 PR
 XX (IMMV) IMMUNEX CORP.
 PA
 XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 PI Rauch C;
 PI
 XX WPI: 1995-373556/48.
 DR
 XX P-PSDB; AAR83309.
 DR
 XX Isolated DNA encoding polypeptide with mammalian IL-15 activity - which
 PT stimulates proliferation and differentiation of T cells, used for
 PT treating carcinoma(s), melanomas, etc. and viral infections
 PT
 XX Claim 2; Page 26; 48pp; English.
 PS
 XX A simian species of IL-15 (sIL-15) was purified and analysed by SDS-
 CC PAGE. Bioassay of unstained gel slices indicated IL-15 activity was
 CC assoc. with proteins having mol. wts in the range of 15-17 kDa. The
 CC N-terminus of the 15-17 kDa was sequenced. The results indicated the
 CC identity of the first 33 AAs of AAR83309. Subsequent sequencing of a
 CC cDNA clone obtd. from a simian library provided a sequence encoding
 CC the polypeptide AAR83436. AAR83436 comprises a relatively short 48 AA
 CC leader sequence and a mature polypeptide AAR83309. The sequence of the
 CC N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers
 CC for the amplification of IL-15-specific DNA sequences. The first
 CC 6 AAs of the N-terminus were used to design one primer, a
 CC degenerate mixture coding for all possible codon usages - AAT00528.
 CC The AA sequences of the simian mature N-terminus 26-31 were used
 CC to design a second primer, a degenerate mixture coding for a
 CC complement of all possible codon usages of AAs 26-31, omitting
 CC posn. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA
 CC cells were used as templates. A 92 bp DNA fragment was used as a
 CC hybridisation probe to screen a portion of a plasmid library contg.
 CC cDNA inserts prepd. from CV-1/EBNA polyadenylated RNA. This
 CC resulted in the isolation of clone C85; sIL-15 that has an ORF
 CC given in AAT00524. AAR83309 is the active polypeptide & AAR83436 is
 CC the precursor polypeptide. AAT00525 encodes the active polypeptide.
 CC
 XX Sequence 345 BP; 124 A; 50 C; 64 G; 107 T; 0 other;
 SQ

Query Match 80.0%; Score 14.4; DB 16; Length 345;
 Best Local Similarity 72.2%; Pred. No. 1.3e+02;
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGGCTNAAYGTNATH 18
 ||:||||| ||:| ||:
 Db 1 aactgggtgaatgtaata 18

RESULT 12
 AAT00527
 ID AAT00527 standard; cDNA: 345 BP.
 XX
 AC AAT00527;
 XX
 DT 02-FEB-1996 (first entry)
 XX
 DE Human interleukin-15 mature polypeptide.
 XX
 KW Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

```

FT      /*tag= 2
FT      /product= "mature sETP"
XX
XX      US6184359-B1.
XX
XX      06-FEB-2001.
XX
XX      09-NOV-1998;    98US-0189193.
XX
XX      22-FEB-1995;    95US-0393305.
XX      04-OCT-1996;    96US-0725969.
XX      08-MAR-1993;    93US-0031399.
XX      22-APR-1994;    94US-0233606.
XX
XX      (IMM ) IMMUNEX CORP.
XX
XX      Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;
XX
XX      WPI: 2001-217801/22.
XX      P-PSDB; AAB62013.
XX
XX      New antibodies that specifically binds epithelium-derived T-cell factor
XX      polypeptide useful for e.g. treating or preventing gastrointestinal
XX      diseases, HIV and HIV-associated diseases, augmenting destruction of
XX      tumour cells -
XX
XX      Disclosure: Fig 1: 35pp; English.
XX
XX      The invention relates to simian and human epithelium-derived T-cell
XX      factor (ETP) polypeptides. Antibodies that specifically bind to the ETP
XX      polypeptides are used for treating or preventing gastrointestinal
XX      diseases, such as chemotherapy and radiation therapy-induced enteritis
XX      and mucositis, peptic ulcer disease, villus atrophic disorders and
XX      inflammatory bowel disease; for increasing tolerated doses for radiation
XX      therapy and chemotherapy agents which are limited by gastrointestinal
XX      toxicity; and for treating HIV and HIV-associated diseases. The
XX      antibodies are further used to treat a variety of other diseases or
XX      conditions where it is desired to stimulate proliferation of
XX      T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B
XX      lymphocytes, to augment anti-infectious disease immunity, to induce CTL,
XX      LAK or NK lytic activity, or to augment the destruction of tumour cells
XX      or cells infected with virus. The present sequence represents a cDNA
XX      encoding the simian ETP (sETP) mature polypeptide.
XX
XX      Sequence 345 BP; 121 A; 49 C; 68 G; 107 T; 0 other:
XX
XX      Query Match      80.0%; Score 14.4; DB 22; Length 345;
XX      Best Local Similarity 72.2%; Pred. No. 1.3e+02;
XX      Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX      QY      1 AAYTGGGTAAAYGTNATH 18
XX      ||:||||| ||:| ||:
XX      Db      1 aactggtgcatgtata 18
XX
XX      RESULT 14
XX      AAF57025
XX      ID AAF57025 standard; cDNA: 345 BP.
XX      XX
XX      AAF57025;
XX
XX      14-MAY-2001 (first entry)
XX
XX      Human ETP (hETP) mature polypeptide encoding cDNA.
XX
XX      Epithelium-derived T-cell factor; ETP; simian; human; enteritis;
XX      gastrointestinal disease; mucositis; peptic ulcer; cytostatic;
XX      villus atrophic disorder; inflammatory bowel disease; anti-inflammatory;
XX      anti-HIV; antiviral; T-lymphocyte stimulator; ss.
XX
XX      Homo sapiens.
XX

```

FH KEY Location/Qualifiers
 FT CDS 1..345 /*tag= a
 FT /product= "mature hETF"
 FT
 PN US6184359-B1.
 PD 06-FEB-2001.
 PD
 PE 09-NOV-1998; 98US-0189193.
 PE
 PR 22-FEB-1995; 95US-0393305.
 PR 04-OCT-1996; 96US-0725969.
 PR 08-MAR-1993; 93US-0031399.
 PR 22-APR-1994; 94US-0233606.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;
 XX
 DR WPI: 2001-217801/22.
 DR P-PSDB: AAB62015.
 XX
 PT New antibodies that specifically binds epithelium-derived T-cell factor
 PT polypeptide useful for e.g. treating or preventing gastrointestinal
 PT diseases, HIV and HTV-associated diseases, augmenting destruction of
 PT tumour cells
 PT
 PS Disclosure: Flg 2: 35pp; English.
 XX
 CC The invention relates to simian and human epithelium-derived T-cell
 CC factor (ETF) polypeptides. Antibodies that specifically bind to the ETF
 CC polypeptides are used for treating or preventing gastrointestinal
 CC diseases, such as chemotherapy and radiation therapy-induced enteritis
 CC and mucositis, peptic ulcer disease, villus atrophic disorders and
 CC inflammatory bowel disease; for increasing tolerated doses for radiation
 CC therapy and chemotherapy agents which are limited by gastrointestinal
 CC toxicity; and for treating HIV and HTV-associated diseases. The
 CC antibodies are further used to treat a variety of other diseases or
 CC conditions where it is desired to stimulate proliferation of
 CC T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B
 CC lymphocytes, to augment anti-infectious disease immunity, to induce CTL,
 CC LAK or NK lytic activity, or to augment the destruction of tumour cells
 CC or cells infected with virus. The present sequence represents a CDNA
 CC encoding the human ETF (hETF) mature polypeptide.
 CC
 CC Sequence 345 BP; 124 A; 50 C; 64 G; 107 T; 0 other;
 CC
 SQ
 Query Match 80.0%; Score 14.4; DB 22; Length 345;
 Best Local Similarity 72.2%; Pred. No. 1.3e+02;
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAYTGGTNAAYGTNATH 18
 ||:||||| ||:|||||
 Db 1 aactgggtgaatgtaata 18
 RESULT 15
 AAF21344
 ID AAF21344 standard; DNA: 486 BP.
 XX
 AC AAF21344;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human low adenosine antisense oligonucleotide related sequence #2911.
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW

KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 XX Homo sapiens.
 OS
 PN WO200062736-A2.
 PN
 PD 26-OCT-2000.
 PD
 PE 24-MAR-2000; 2000WO-US08020.
 PE
 PR 06-APR-1999; 99US-0127958.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 XX (NYCE/) NYCE J W.
 PA
 PI Nyce JW;
 XX
 DR WPI: 2000-679539/66.
 DR
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions
 PT
 PS Disclosure: Page 1348-1349; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, central
 CC chemo-kine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system peptide
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 CC
 CC Sequence 486 BP; 154 A; 81 C; 100 G; 151 T; 0 other;
 CC
 SQ
 Query Match 80.0%; Score 14.4; DB 21; Length 486;
 Best Local Similarity 72.2%; Pred. No. 1.3e+02;
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAYTGGTNAAYGTNATH 18
 ||:||||| ||:|||||
 Db 123 aactgggtgaatgtaata 140

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RESULT 15
 US-08-794-524-12/c
 ; Sequence 12, Application US/08794524
 ; Patent No. 5985262
 ; GENERAL INFORMATION:
 ; APPLICANT: Grabstein, Kenneth
 ; APPLICANT: Anderson, Dirk
 ; APPLICANT: Eisenman, June
 ; APPLICANT: Fung, Victor
 ; APPLICANT: Rauch, Charles
 ; TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/794,524
 ; FILING DATE: 03-FEB-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/393,305
 ; FILING DATE: 22-FEB-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mcmasters, David D.
 ; REGISTRATION NUMBER: 33,963
 ; REFERENCE/DOCKET NUMBER: 480052.409C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-622-4900
 ; INFORMATION FOR SEQ. ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 345 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..345
 ; US-08-794-524-12

Query Match 84.7%; Score 14.4; DB 2; Length 345;
 Best Local Similarity 70.6%; Pred. No. 21;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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DB	92	ACATCACTTTCCTATA	76

Search completed: June 19, 2002, 02:22:12
 Job time: 5420 sec

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..345
US-08-726-817-13

Query Match 84.7%; Score 14.4; DB 1; Length 345;
Best Local Similarity 70.6%; Pred. No. 21;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRCTCTCTCTCTCTA 17
11:11:11:11:11:11
DB 92 ACATCACTTCTGTATA 76

RESULT 13
US-08-725-969-12/c
Sequence 12, Application US/08725969
Patent No. 5892001
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,969
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..345
US-08-725-969-12

Query Match 84.7%; Score 14.4; DB 2; Length 345;
Best Local Similarity 70.6%; Pred. No. 21;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRCTCTCTCTCTCTA 17
11:11:11:11:11:11
DB 92 ACATCACTTCTGTATA 76

RESULT 14
US-08-725-969-13/c
Sequence 13, Application US/08725969
Patent No. 5892001
GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,969
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..345
US-08-725-969-13

Query Match 84.7%; Score 14.4; DB 2; Length 345;
Best Local Similarity 70.6%; Pred. No. 21;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRCTCTCTCTCTCTA 17
11:11:11:11:11:11
DB 92 ACATCACTTCTGTATA 76

QY 1 ACRTGCTYTCNGTGRA 17
11:11:11:11:11
DB 92 ACATCACTTCCGTATA 76

RESULT 10

US-08-393-305-13/c

Sequence 13, Application US/08393305

Patent No. 5574138

GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth

APPLICANT: Anderson, Dirk

APPLICANT: Eisenman, June

APPLICANT: Fung, Victor

APPLICANT: Rauch, Charles

TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/393,305

FILING DATE: 22-FEB-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Mcmasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 480052.409C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 345 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 1..345

US-08-393-305-13

Query Match 84.7%; Score 14.4; DB 1; Length 345;

Best Local Similarity 70.6%; Pred. No. 21;

Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACRTGCTYTCNGTGRA 17
11:11:11:11:11

DB 92 ACATCACTTCCGTATA 76

RESULT 11

US-08-726-817-12/c

Sequence 12, Application US/08726817

Patent No. 5707616

GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth

APPLICANT: Anderson, Dirk

APPLICANT: Eisenman, June

APPLICANT: Fung, Victor

APPLICANT: Rauch, Charles

TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726,817

FILING DATE: 04-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/393,305

FILING DATE: 22-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: Mcmasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 480052.409C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 345 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 1..345

US-08-726-817-12

Query Match 84.7%; Score 14.4; DB 1; Length 345;

Best Local Similarity 70.6%; Pred. No. 21;

Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACRTGCTYTCNGTGRA 17
11:11:11:11:11

DB 92 ACATCACTTCCGTATA 76

RESULT 12

US-08-726-817-13/c

Sequence 13, Application US/08726817

Patent No. 5707616

GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth

APPLICANT: Anderson, Dirk

APPLICANT: Eisenman, June

APPLICANT: Fung, Victor

APPLICANT: Rauch, Charles

TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726,817

FILING DATE: 04-OCT-1996

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,193
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-189-193-11

Query Match      84.7%; Score 14.4; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTCRCTYTCNGTRTA 17
   |||||
Db 1 ACRTCRCTYTCNGTRTA 17

RESULT 8
PCT-US94-03793-11
Sequence 11, Application PC/TUS9403793
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: Interleukin-15
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03793
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: launer, Charlene
REGISTRATION NUMBER: 33,035
```

```

REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
PCT-US94-03793-11

Query Match      84.7%; Score 14.4; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTCRCTYTCNGTRTA 17
   |||||
Db 1 ACRTCRCTYTCNGTRTA 17

RESULT 9
US-08-393-305-12/C
Sequence 12, Application US/08393305
Patent No. 5574138
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,305
FILING DATE: 22-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..345
US-08-393-305-12

Query Match      84.7%; Score 14.4; DB 1; Length 345;
Best Local Similarity 70.6%; Pred. No. 21;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-504-042-11

Query Match 84.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTCTCTTCNGTCTTA 17
|||||
Db 1 ACRTCTCTTCNGTCTTA 17

RESULT 5
US-08-725-969-11
Sequence 11, Application US/08725969
Patent No. 5892001
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
ATTORNEY/AGENT INFORMATION:
APPLICANT: Eisenman, June
APPLICANT: Funf, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELUM-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,969
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-725-969-11

Query Match 84.7%; Score 14.4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTCTCTTCNGTCTTA 17
|||||
Db 1 ACRTCTCTTCNGTCTTA 17

RESULT 6
US-08-794-524-11
Sequence 11, Application US/08794524
Patent No. 5985262
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
ATTORNEY/AGENT INFORMATION:
APPLICANT: Eisenman, June
APPLICANT: Funf, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELUM-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,524
FILING DATE: 03-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-794-524-11

Query Match 84.7%; Score 14.4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTCTCTTCNGTCTTA 17
|||||
Db 1 ACRTCTCTTCNGTCTTA 17

RESULT 7
US-09-189-193-11
Sequence 11, Application US/09189193
Patent No. 6184359
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
ATTORNEY/AGENT INFORMATION:
APPLICANT: Eisenman, June
APPLICANT: Funf, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELUM-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15

SOURCE Tetraodon nigroviridis.
 ORGANISM Tetraodon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodon.
 REFERENCE 1 (bases 1 to 939)
 AUTHORS Roest-Crolius,H., Jallion,O., Dasilva,C., Fzames,C., Fisher,C.,
 Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
 Weissenbach,J.
 TITLE Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 939)
 AUTHORS Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fzames,C., Winkler,P., Brotlier,P., Quetier,F.,
 Saurin,W. and Weissenbach,J.
 TITLE Human gene number estimate provided by genome wide analysis using
 Tetraodon nigroviridis DNA sequence
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 939)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
 COMMENT This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetraodon nigroviridis
 genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetraodon>.
 FEATURES
 source
 1..939
 /organism="Tetraodon nigroviridis"
 /db_xref="taxon:99883"
 /clone="181K04"
 /clone_1lb="g"
 /note="Genoscope sequence ID : COAG181BF02SP1-end :
 PUC-Or1"
 BASE COUNT 244 a 218 c 215 g 249 t 13 others
 ORIGIN
 Query Match 84.7%; Score 14.4; DB 12; Length 939;
 Best Local Similarity 70.6%; Pred. No. 2e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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 ||:||||:||||:|
 Db 599 ACRTGCTCTGCTGTGA 583

Search completed: June 19, 2002, 02:15:56
 Job time: 7369 sec

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4447957"
 /clone_lib="NIH_MGC_89"
 /tissue_type="hypernephroma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.3 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

BASE COUNT

237 a 173 c 177 g 236 t

Query Match 84.7%; Score 14.4; DB 10; Length 823;
 Best Local Similarity 70.6%; Pred. No. 1.9e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTCTCTTCNGTCTA 17
 11:11:11:11:11:11
 Db 593 ACATCCTTCTCGTGA 609

RESULT 13
 B1758686/c 872 bp mRNA linear EST 25-SEP-2001
 LOCUS 603024240F1 NIH_MGC_114 Homo sapiens CDNA IMAGE:5194977 5',
 DEFINITION mRNA sequence.
 ACCESSION B1758686
 VERSION B1758686.1 GI:15750264
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 872)
 NIH-MGC http://mhc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M11487 row: o column: 10
 High quality sequence start: 24
 Location/Qualifiers

FEATURES

1..872

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5194977"
 /clone_lib="NIH_MGC_114"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:
 this is a NIH_MGC Library."
 BASE COUNT 200 a 222 c 227 g 223 t
 ORIGIN

Query Match

84.7%; Score 14.4; DB 10; Length 872;

Best Local Similarity 70.6%; Pred. No. 1.9e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTCTCTTCNGTCTA 17
 11:11:11:11:11:11
 Db 828 ACATCCTTCTCGTGA 812

RESULT 14
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 LOCUS SP_0097_B2.G11.SPEE Strongylocentrotus purpuratus, purple sea
 urchin, sperm genomic BAC library Strongylocentrotus purpuratus
 genomic clone Plate=97 Col=22 Row=N, DNA sequence.
 ACCESSION A2204912
 VERSION A2204912.1 GI:8399832
 KEYWORDS GSS.
 SOURCE Strongylocentrotus purpuratus.
 ORGANISM Strongylocentrotus purpuratus.
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinoidea; Euechinozoa; Echinodermata; Echinodermata;
 Strongylocentrotidae; Strongylocentrotus.
 1 (bases 1 to 935)
 Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Blondi,T.R.,
 Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,
 G.A., Eitensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and
 Hood,L.
 A sea urchin genome project: Sequence scan, virtual map, and
 additional resources
 Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
 20402566
 COMMENT Division of Biology 156-29
 California Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047
 Email: acameron@caltech.edu
 Plate: 97 row: N column: 22
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 935.
 Location/Qualifiers

FEATURES

1..935

/organism="Strongylocentrotus purpuratus"
 /db_xref="taxon:7668"
 /clone="Plate=97 Col=22 Row=N"
 /clone_lib="Strongylocentrotus purpuratus, purple sea
 urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BACs; BAC Clones in E-Coli
 DH10B"
 BASE COUNT 261 a 171 c 170 g 333 t
 ORIGIN

Query Match 84.7%; Score 14.4; DB 12; Length 935;
 Best Local Similarity 70.6%; Pred. No. 2e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTCTCTTCNGTCTA 17
 11:11:11:11:11:11
 Db 497 ACATCCTTCTCGTGA 513

RESULT 15
 CNS02YU0 939 bp DNA linear GSS 15-MAY-2000
 LOCUS Tetradon nigroviridis genome survey sequence pUC-Or1 end of clone
 181k04 of library G from Tetradon nigroviridis, genomic survey
 sequence.
 ACCESSION AL220113
 VERSION AL220113.1 GI:7878932
 KEYWORDS GSS; genome survey sequence.

Library constructed by Life Technologies. Investigator
 Providing samples: Gilbert Smith, NIH

BASE COUNT 139 a 280 c 179 g 193 t

Query Match 84.7%; Score 14.4; DB 10; Length 791;
 Best Local Similarity 70.6%; Pred. No. 1.8e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTCRCTTCNGTGA 17
 11:11:11:11:11:11

Db 530 ACATCACTTCGTGTA 546

RESULT 10
 BG184658 800 bp mRNA linear EST 21-APR-2001
 LOCUS
 DEFINITION RST3720 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 ACCESSION BG184658
 VERSION BG184658.1 GI:13706473
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 800)
 Harrington, J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
 Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J.,
 Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,
 'E., Veloso, N., Kika, A., Hess, J., Coluren, K., Lo, K., Offenbacher,
 'J., Danzig, J., and Ducar, M.
 Creation of genome-wide protein expression libraries using random
 activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)

TITLE
 JOURNAL MEDLINE
 COMMENT
 Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scaine@atersys.com
 High quality sequence stop: 444.

FEATURES
 Source
 Location/Qualifiers
 1..800
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression
 Libraries using Random Activation of Gene Expression',
 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."

BASE COUNT 235 a 151 c 165 g 247 t

Query Match 84.7%; Score 14.4; DB 10; Length 800;
 Best Local Similarity 70.6%; Pred. No. 1.8e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTCRCTTCNGTGA 17
 11:11:11:11:11:11

Db 500 ACATCACTTCGTGTA 484

RESULT 11
 BH551681 816 bp DNA linear GSS 14-DEC-2001
 LOCUS
 DEFINITION BOCIY81YR BOGL Brassica oleracea genomic clone BOCIY81, DNA
 sequence.

ACCESSION BH551681
 VERSION BH551681.1 GI:17803461
 KEYWORDS GSS.
 SOURCE Brassica oleracea.
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 816)
 Town, C.D., Van Aken, S., Utterback, T., and Fraser, C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 unpublished (2001)
 JOURNAL
 COMMENT
 Other GSS: BOCIY81TF
 Contact: Chris Town

TIGR Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.

FEATURES
 Source
 Location/Qualifiers
 1..816
 /organism="Brassica oleracea"
 /strain="T01000DH3"
 /db_xref="taxon:3712"
 /clone_lib="BOGLY81"
 /clone_lib="BOGLY81"
 /note="Vector: PHOS1. Site 1: BstXI. 2-3 kb sheared
 genomic DNA inserted into PHOS1 using BstXI linkers"

BASE COUNT 257 a 192 c 176 g 191 t

Query Match 84.7%; Score 14.4; DB 12; Length 816;
 Best Local Similarity 70.6%; Pred. No. 1.9e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTCRCTTCNGTGA 17
 11:11:11:11:11:11

Db 530 ACATCACTTCGTGTA 514

RESULT 12
 BG167809 823 bp mRNA linear EST 06-FEB-2001
 LOCUS
 DEFINITION 602333995P1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4447957 5',
 mRNA sequence.
 ACCESSION BG167809
 VERSION BG167809.1 GI:12674512
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 823)
 NIH-MGC http://mgs.nci.nih.gov/.
 TITLE
 JOURNAL
 COMMENT
 Contact: Robert Strusberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LLM10229 row: 1 column: 14
 High quality sequence stop: 645.

FEATURES
 Source
 Location/Qualifiers
 1..823

BG675661
 LOCUS 756 bp mRNA linear EST 01-MAY-2001
 DEFINITION 602622072F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4747265 5',
 mRNA sequence.
 ACCESSION BG675661
 VERSION BG675661.1 GI:13907057
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 756)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM10596 row: p column: 18
 High quality sequence stop: 745.
 Location/Qualifiers
 1..756
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="4747265"
 /clone_lib="NCI_CGAP_Skn4"
 /tissue_type="squamous cell carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 221 a 147 c 168 g 220 t
 ORIGIN
 Query Match 84.7% Score 14.4; DB 10; Length 756;
 Best Local Similarity 70.6%; Pred. No. 1.8e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 ACRTCRCTTCNGTCTA 17
 ||:||||:||||:||||
 Db 710 ACATCAGCTCTCGATATA 726
 RESULT 8
 BI832895 756 bp mRNA linear EST 04-OCT-2001
 LOCUS 603082478F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5221771 5',
 mRNA sequence.
 ACCESSION BI832895
 VERSION BI832895.1 GI:15944445
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 756)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM11557 row: k column: 20
 High quality sequence stop: 756.
 Location/Qualifiers
 1..756
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="5221771"
 /clone_lib="NIH_MGC_120"
 /lab_host="DH10B"
 /note="Organ: pooled pancreas and spleen; Vector:
 pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of spleen and pancreas from 28 yo
 male. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 1.5 kb. Insert size range 1-2.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 025. Note: this is a NIH-MGC Library."
 BASE COUNT 247 a 115 c 143 g 251 t
 ORIGIN
 Query Match 84.7% Score 14.4; DB 10; Length 756;
 Best Local Similarity 70.6%; Pred. No. 1.8e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 ACRTCRCTTCNGTCTA 17
 ||:||||:||||:||||
 Db 63 ACATCAGCTTCGATATA 47
 RESULT 9
 BE380693 791 bp mRNA linear EST 21-JUL-2000
 LOCUS 601270690F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3599950 5',
 mRNA sequence.
 ACCESSION BE380693
 VERSION BE380693.1 GI:9325968
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 791)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM8783 row: c column: 23
 High quality sequence stop: 51.
 Location/Qualifiers
 1..791
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone_image="3599950"
 /clone_lib="NCI_CGAP_Mam1"
 /tissue_type="tumor, biopsy sample"
 /dev_stage="10 months, virgin"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraiki
 Toshlyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM10752 row: 0 column: 20
 High quality sequence stop: 630.
 Location/Qualifiers

FEATURES

source

1..643
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:4830955"
 /clone_lib="NIH_MGC_97"
 /lab_host="DH10B"
 /note="Organ: testis; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3',
 size-selected for average insert size 2.2 kb and
 normalized to R0T 5. This is a primary library enriched
 for full-length clones and constructed using the
 cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIH/NHGRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT

161 a 165 c 160 g 157 t

ORIGIN

Query Match 84.7%; Score 14.4; DB 10; Length 643;
 Best Local Similarity 70.6%; Pred. No. 1.7e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATCCTCTCCGTATA 17

Db 340 ACATCCTCTCCGTATA 324

RESULT 5

LOCUS

AU211793 673 bp mRNA linear EST 17-JUL-2001
 AU211793 unpublished oligo-capped cDNA library, stage L2

DEFINITION

Caenorhabditis elegans cDNA clone yk776g02 3', mRNA sequence.

ACCESSION

AU211793

VERSION

AU211793.1

KEYWORDS

EST.

SOURCE

Caenorhabditis elegans.

ORGANISM

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae

REFERENCE

1 (bases 1 to 673)

AUTHORS

Kohara,Y., Shih-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.

TITLE

A complementary view of the C.elegans genome

JOURNAL

Unpublished (2001)

COMMENT

Contact: Yuji Kohara
 Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykohara@lab.nig.ac.jp.
 Location/Qualifiers

FEATURES

1..673

source

/organism="Caenorhabditis elegans"
 /strain="N2"
 /db_xref="taxon:6239"
 /clone_image="YK776g02"
 /clone_lib="unpublished oligo-capped cDNA library, stage
 L2"

/sex="Hermaphrodite"

/tissue_type="whole animal"

/dev_stage="L2"

BASE COUNT 188 a 139 c 125 g 219 t 2 others

ORIGIN

Query Match 84.7%; Score 14.4; DB 9; Length 673;
 Best Local Similarity 70.6%; Pred. No. 1.7e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATCCTCTCCGTATA 17

Db 455 ACATCCTCTCCGTATA 471

RESULT 6

LOCUS

AG091422 735 bp DNA linear GSS 03-NOV-2001
 AG091422 Pan troglodytes DNA, clone: PTB-091E11.R, genomic survey sequence.

DEFINITION

AG091422

ACCESSION

AG091422.1

VERSION

GSS: GSS (genome survey sequence).

KEYWORDS

Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male

SOURCE

BAC library clone:PTB-091E11.R.

ORGANISM

Pan troglodytes

REFERENCE

1 (sites)

Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

Totokl,Y., Watanabe,H. and Sakaki,Y.

BAC end sequences of library PTB

Unpublished

2 (bases 1 to 735)

Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

Totokl,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

Submitted (02-NOV-2001) Asao Fujiyama, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suenho-chou,Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/)

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end

clones were generated during the R&D process and may have higher chance of

clone tracking errors.

PRIMERS
 Sequencing: M13Rev

LIBRARY

Vector : PKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1..735

/organism="Pan troglodytes"

/db_xref="taxon:9598"

/clone_image="PTB-091E11.R"

/sex="male"

/cell_type="lymphoblast"

/clone_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT

239 a 184 c 95 g 217 t

ORIGIN

Query Match 84.7%; Score 14.4; DB 12; Length 735;
 Best Local Similarity 70.6%; Pred. No. 1.8e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATCCTCTCCGTATA 17

Db 211 ACATCCTCTCCGTATA 227

RESULT 7

/lab_host="DH10B"
 /note="Organ: mixed (see below); Vector: pT73D-Pac
 (Pharmacia) with a modified polylinker; Site_1: Not I;
 Site_2: Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NDH, pregnant uterus
 NBHPU, and fetal heart NBH19W) were mixed, and ss circles
 were made in vitro. Following HAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."

BASE COUNT 149 a 91 c 108 g 161 t

ORIGIN

Query Match 84.7%; Score 14.4; DB 9; Length 509;
 Best Local Similarity 70.6%; Pred. No. 1.5e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACRTRCTYTCNGTATA 17
 11:11:11:11:11:11

DB 340 ACATCACTTCGCTATA 324

RESULT 2
 LOCUS A1860008 637 bp mRNA linear EST 07-MAR-2000
 DEFINITION wM22903.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2436724 3'
 similar to SW:IL15_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ; mRNA
 sequence.
 ACCESSION A1860008
 VERSION A1860008.1 GI:5513624
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 637)
 NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-rt@mail.nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILM at:
 www.bio.liml.gov/dbtrp/image/image.html
 Insert Length: 3944 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 410.

FEATURES
 Source

1 - 637
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:2436724"
 /clone_lib="NCI_CGAP_Ut4"
 /tissue_type="serous papillary carcinoma, high grade, 2
 pooled tumors"
 /lab_host="DH10B"
 /note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.48 kb. Life Technologies catalog #:
 11542-016"

BASE COUNT 207 a 111 c 91 g 227 t 1 others

ORIGIN

Query Match 84.7%; Score 14.4; DB 9; Length 637;
 Best Local Similarity 70.6%; Pred. No. 1.7e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACRTRCTYTCNGTATA 17
 11:11:11:11:11:11

DB 591 ACATCACTTCGCTATA 607

RESULT 3
 LOCUS BJ144320 641 bp mRNA linear EST 23-JAN-2002
 DEFINITION BJ144320 unpublished oligo-capped cDNA library, C. elegans L1 stage
 Caenorhabditis elegans cDNA clone yk1205h10 3', mRNA sequence.
 ACCESSION BJ144320
 VERSION BJ144320.1 GI:18304486
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae
 ; Rhabditidae; Peleoderinae; Caenorhabditis.
 1 (bases 1 to 641)
 Kohara, Y., Shin, I.T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
 and Sugano, S.
 A complementary view of the C. elegans genome
 Unpublished (2002)
 TITLE Center for Genetic Resource Information
 JOURNAL National Institute of Genetics
 COMMENT 1111 Yata, M. Shima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genetics.nig.ac.jp.

FEATURES
 Source

1 - 641
 /organism="Caenorhabditis elegans"
 /strain="N2"
 /db_xref="taxon:6239"
 /clone_image="yk1205h10"
 /clone_lib="unpublished oligo-capped cDNA library, C.
 elegans L1 stage"
 /sex="hermaphrodite"
 /tissue_type="whole animal"
 /dev_stage="L1"

BASE COUNT 183 a 133 c 114 g 209 t 2 others

ORIGIN

Query Match 84.7%; Score 14.4; DB 10; Length 641;
 Best Local Similarity 70.6%; Pred. No. 1.7e+03;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACRTRCTYTCNGTATA 17
 11:11:11:11:11:11

DB 443 ACATCACTTCGCTATA 459

RESULT 4
 LOCUS BG722010 643 bp mRNA linear EST 08-MAY-2001
 DEFINITION BG722010 602698780F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4830955 5',
 mRNA sequence.
 ACCESSION BG722010
 VERSION BG722010.1 GI:14001197
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 643)
 NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 02:15:53 ; Search time 2591.91 Seconds
(without alignments)
88.525 Million cell updates/sec

Title: US-09-724-841-11

Sequence: 1 ACRRCRCRYTCNGTRTA 17

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estlin: *
4: em_estnu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hlc: *
9: gb_estl: *
10: gb_estl2: *
11: gb_hlc: *
12: gb_gss: *
13: em_gss_hum: *
14: em_gss_liv: *
15: em_gss_pln: *
16: em_gss_vrt: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
C	1	14.4	84.7	509	9	AA463370	zx97d12.r	AA463370 zx97d12.r
C	2	14.4	84.7	637	9	AI860008	wm22903.x	AI860008 wm22903.x
C	3	14.4	84.7	641	10	BJ144320	BJ144320	BJ144320 BJ144320
C	4	14.4	84.7	643	10	BG722010	602698780	BG722010 602698780
C	5	14.4	84.7	673	9	AU211793	AU211793	AU211793 AU211793
C	6	14.4	84.7	735	12	AG091422	Pan trogl	AG091422 Pan trogl
C	7	14.4	84.7	756	10	BG675661	603082478	BG675661 603082478
C	8	14.4	84.7	756	10	BI832895	603082478	BI832895 603082478
C	9	14.4	84.7	791	10	BE380693	601270690	BE380693 601270690
C	10	14.4	84.7	800	10	BG184658	RST3720.A	BG184658 RST3720.A
C	11	14.4	84.7	816	12	BH551681	BG167809	BH551681 BG167809
C	12	14.4	84.7	823	10	BG167809	602339953	BG167809 602339953
C	13	14.4	84.7	872	10	BI758686	603024240	BI758686 603024240
C	14	14.4	84.7	935	12	AZ204912	SP_0097_B	AZ204912 SP_0097_B
C	15	14.4	84.7	939	12	CNS02YU0	tetradon	AZ204912 tetradon
C	16	14.4	84.7	973	9	BB612210	BB612210	BB612210 BB612210
C	17	14.4	84.7	982	9	AL548180	AL548180	AL548180 AL548180

C	18	14.4	84.7	989	12	CNS065ZW	AL413922 T7 end of	AL413922 T7 end of
C	19	14.4	84.7	994	9	AL572832	AL572832	AL572832
C	20	14.4	84.7	1039	10	BG111302	BG111302 602283384	BG111302 602283384
C	21	14.4	84.7	1937	10	BE686933	602102705	BE686933 602102705
C	22	13.4	78.8	169	10	R30748	R30748 F9864 fetal	R30748 F9864 fetal
C	23	13.4	78.8	190	10	BG000197	RC3-GN002	BG000197 RC3-GN002
C	24	13.4	78.8	192	12	AO647900	RPCT193-DP	AO647900 RPCT193-DP
C	25	13.4	78.8	237	12	A2737501	RPCT-24-1	A2737501 RPCT-24-1
C	26	13.4	78.8	254	9	AV209229	AV209229	AV209229
C	27	13.4	78.8	259	9	AV157396	u56508.Y	AV157396 u56508.Y
C	28	13.4	78.8	273	9	AI578096	AI578096 UI-R-C3-L	AI578096 UI-R-C3-L
C	29	13.4	78.8	273	9	AM530109	UI-R-C4-a	AM530109 UI-R-C4-a
C	30	13.4	78.8	284	9	AA684293	vm54b09.r	AA684293 vm54b09.r
C	31	13.4	78.8	285	9	AV155882	AV155882	AV155882
C	32	13.4	78.8	289	9	AA762984	vw58e08.r	AA762984 vw58e08.r
C	33	13.4	78.8	294	9	AV339187	AV339187	AV339187
C	34	13.4	78.8	307	10	BG608621	BG608621 307261 MA	BG608621 307261 MA
C	35	13.4	78.8	307	10	BM483899	537518 MA	BM483899 537518 MA
C	36	13.4	78.8	308	9	AM786829	120399 MA	AM786829 120399 MA
C	37	13.4	78.8	328	12	AO651927	Sheared D	AO651927 Sheared D
C	38	13.4	78.8	337	10	BM484651	BM484651 538578 MA	BM484651 538578 MA
C	39	13.4	78.8	335	9	AU203535	AU203535	AU203535
C	40	13.4	78.8	360	9	AV187535	AV187535	AV187535
C	41	13.4	78.8	360	9	AV195907	AV195907	AV195907
C	42	13.4	78.8	369	9	AA826842	nr90a04.s	AA826842 nr90a04.s
C	43	13.4	78.8	374	10	BM133541	NXLV_008-	BM133541 NXLV_008-
C	44	13.4	78.8	378	10	BE692792	SAC294 Mo	BE692792 SAC294 Mo
C	45	13.4	78.8	390	12	AQ166959	HS_3148_B	AQ166959 HS_3148_B

ALIGNMENTS

RESULT 1
AA463370/c
LOCUS
DEFINITION
AA463370 509 bp mRNA linear EST 10-JUN-1997
zx97d12.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811703 5'
similar to SW:IL15_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ; mRNA
sequence.
ACCESSION
AA463370
VERSION
AA463370.1 GI:2188254
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 509)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, R., Steptoe, M., Tan, F., Theisling, B., White, Y., Wyllie,
T., Waterston, R. and Wilson, R.
Washu-Merck EST Project 1997
TITLE
Unpublished (1997)
JOURNAL
Contact: Wilson RK
COMMENT
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -28m3 rev2 ET from Amersham
High quality sequence stop: 416.
Location/Qualifiers
1. 509
/organism="Homo sapiens"
/db_xref="GDB:6042614"
/db_xref="taxon:9606"
/clone="IMAGE:811703"
/clone_lib="Soares_NHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"

FEATURES

source

CC leader sequence and a mature polypeptide AAR83309. The sequence of the
 CC N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers
 CC for the amplification of IL-15-specific DNA sequences. The first
 CC 6 AAs of the N-terminus were used to design one primer, a
 CC degenerate mixture coding for all possible codon usages - AAT00528.
 CC The AA sequences of the simian mature N-terminus 26-31 were used
 CC to design a second primer, a degenerate mixture coding for a
 CC complement of all possible codon usages of AAs 26-31, omitting
 CC posn. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA
 CC cells were used as templates. A 92 bp DNA fragment was used as a
 CC hybridism. probe to screen a portion of a plasmid library contg.
 CC cDNA inserts prep'd. from CV-1/EBNA polyadenylated RNA. This
 CC resulted in the isolation of clone C85-STL-15 that has an ORF
 CC given in AAT00524. AAR83309 is the active polypeptide & AAR83436 is
 CC the precursor polypeptide.
 XX

SQ Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match 84.7%; Score 14.4; DB 16; Length 489;
 Best Local Similarity 70.6%; Pred. No. 1.1e+02;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACRTGRCCTCTGNGTRTA 17
 ||:||||:||||:|
 DB 236 ACATCAGTTCTGTATTA 220

Search completed: June 19, 2002, 02:20:52
 Job time: 5410 sec

CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.

XX Sequence 486 BP; 154 A; 81 C; 100 G; 151 T; 0 other;

SO

Query Match 84.7%; Score 14.4; DB 21; Length 486;
Best Local Similarity 70.6%; Pred. No.1.le+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0.

OY 1 ACRRCRCCTTCNGTRPA 17
||:|:|:|:|:|:|:|:|
DB 214 ACATCACCTTCGCTATA 198

RESULT 14
AAA35222/c
ID AAA35222 standard; DNA: 486 BP.
XX
AC AAA35222;
XX
XX 28-JUL-2000 (first entry)
DE Human adenosine receptor related polynucleotide 2nd SRQ ID NO:96.
XX
XX Human: adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphocholate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antisthmatic; cytosolic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; Leukemia; lymphoma; carcinoma; metastasis; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200009525-A2.
PN
XX
XX 24-FEB-2000.
PD
XX
XX 03-AUG-1999; 99WO-US17712.
PE
XX
XX 03-AUG-1998; 98US-0095212.
PR
XX
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX
XX Myce JW;
PI
XX
XX WPI: 2000-205971/18.
DR
XX
XX

PS Disclosure: Page 1264; 1343pp: English.

XX The present invention describes a new composition comprising an
XX antisense oligonucleotide (ON) with low adenosine (up to 15%), which
XX targets nucleic acids involved in bronchoconstriction, allergies, and/or
XX inflammation. The ON can have antiinflammatory, antiallergic,
XX antisthmatic, cytosolic and analgesic activities. The compositions are
XX useful for the treatment of diseases associated with inflammation,
XX impaired airways, including lung disease and diseases whose secondary
XX effects afflict the lungs of a subject. They can be used for treating
XX e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
XX asthma, impaired respiration, respiratory distress syndrome, pain, cystic
XX fibrosis, pulmonary hypertension, emphysema, chronic obstructive
XX pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
XX carcinomas, and cancers which may metastasize to the lungs, including
XX breast and prostate cancer. The reduction of the adenosine content of
XX the ONs reduces side effects. The A-containing ONs break down with the
XX release of deoxyadenosine which activates adenosine receptors causing

CC	broadlyconstituted and inflammation. AAA32313 to AAA35312 represent the
CC	nucleotide sequences given in the sequence listing from the present
CC	invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC	185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC	differ from the previously named sequences. SEQ ID NO:11 to 1680
CC	(AAA32323 to AAA33992) are specifically claimed ONS from the present
CC	invention. N.B. Sequences given in the disclosure of the present
CC	invention do not match up with their corresponding SEQ ID NO: sequences
CC	given in the sequence listing.
XX	
SO	Sequence 486 BP; 154 A; 81 C; 100 G; 151 T; 0 other;
QY	
Db	Query Match 84.7%; Score 14.4; DB 21; Length 486; Best Local Similarity 70.6%; Pred. No. 1.1e+02; Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY	1 ACRTGCTGTCNGTPTA 17 : : : 214 ACATCATCTTCGCTATA 198
RESULT 15	
AA00524/c	
ID	AA00524 standard; cDNA: 489 BP.
AC	AA00524;
XX	
DT	02-FEB-1996 (first entry)
XX	
DE	Simian interleukin-15 precursor.
XX	
KW	Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.
XX	
XX	Cebus apella.
XX	
FT	Key Location/Qualifiers
FT	CDS 1..489
FT	/*tag= a
FT	/note= "Claimed"
FT	misc_feature 145..489
FT	/*tag= b
FT	/note= "Claimed"
XX	
PN	W09527722-A.
XX	
PD	19-OCT-1995.
XX	
PF	06-APR-1994; 94WO-US03793.
XX	
PR	06-APR-1994; 94WO-US03793.
XX	
PA	(IMMV) IMMUNEX CORP.
XX	
PI	Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI	Rauch C;
XX	
DR	WPI; 1995-373556/48.
XX	
DR	P-PSDB; AAR83436.
XX	
PT	Isolated DNA encoding polypeptide with mammalian IL-15 activity - which
PT	stimulates proliferation and differentiation of T cells, used for
PT	treating carcinoma(s), melanomas, etc. and viral infections
XX	
PS	Claim 28; Page 26; 48pp; English.
XX	
CC	A simian species of IL-15 (sIL-15) was purified and analysed by SDS-
CC	PAGE. Bioassay of unstained gel slices indicated IL-15 activity was
CC	assoc. with proteins having mol. wts in the range of 15-17 kDa. The
CC	N-terminus of the 15-17 kDa was sequenced. The results indicated the
CC	identity of the first 33 AAs of AAR83309. Subsequent sequencing of a
CC	cDNA clone obt'd. from a simian library provided a sequence encoding
CC	the polypeptide AAR83436. AAR83436 comprises a relatively short 48 AA

Query Match	Best Local Similarity	Matches	Score 14.4;	DB 22;	Length 345;
			Pred. No. 1e+02;	Mismatches 4;	Indels 1;
				Gaps 0;	
1 ACRGCRCTTCNGRTA 17	84.7%;	70.6%;	4;	1;	0;
92 ACATCACTTCGTATA 76					

RESULT	13
AAAF21344/c	
ID	AAAF21344 standard; DNA; 486 BP.
XX	
AC	
XX	AAAF21344;
DT	14-MAR-2001 (first entry)
XX	
DE	Human low adenosine antisense oligonucleotide related sequence #2911.
XX	
KW	low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW	human; airway disorder; bronchoconstriction; lung inflammation;
KW	surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW	immunosuppressive; antialstatic; analgesic; hypotensive; cyostatic;
KW	respiratory obstruction; pulmonary obstruction; impeded respiration;
KW	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis
KW	pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW	cancer; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO20062736-A2.
XX	
PD	26-OCT-2000.
XX	
PF	24-MAR-2000; 2000WO-US08020.
XX	
PR	06-APR-1999; 99US-0127958.
XX	
PA	(UYEC-) UNIV EAST CAROLINA.
PA	(NYCE/) NYCE J W.
XX	
PI	Nyce JW;
XX	
DR	WPI, 2000-679539/66.
XX	
PT	Low adenosine (A) content antisense oligonucleotides which do not
PT	trigger adenosine receptors during metabolism, useful e.g. for treating
PT	cancers and respiratory obstructions -
PS	Disclosure: Page 1348-1349; 1592p; English.
XX	
XX	
CC	The present invention describes low adenosine (A) content antisense
CC	oligonucleotides and compositions (i) comprising them. In the antisense
CC	oligonucleotides the A is replaced by a 'Universal' or alternative base
CC	(i) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC	immunosuppressive, antialstatic, hypotensive and cyostatic activities
CC	The antisense oligonucleotides and (i) can be used to down-regulate the
CC	expression and or activity of target polypeptides associated with
CC	lung/respiratory disorders and malignancies, such as stimulating and
CC	activating peptide factors and transmitters, transcription factors,
CC	immunoglobulins and antibodies, antibody receptors, cytokines and
CC	chemokines, endogenously produced specific and non-specific enzymes,
CC	binding proteins, adhesion molecules and their receptors, cytokine and
CC	chemokine receptors, adenosine receptors, bradykinin receptors, central
CC	nervous system (CNS) and peripheral nervous and non-nervous system
CC	receptors, CNS and peripheral nervous and non-nervous system peptide
CC	transmitters, defensins, growth factors, vasoactive peptides and
CC	transmitters, binding proteins and malignancy associated proteins. The
CC	antisense oligonucleotides may be used in this way to treat disorders
CC	including respiratory obstruction (especially pulmonary obstruction
CC	and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC	and/or surfactant hypoproduction which are associated with a disease or
CC	condition selected from pulmonary vasoconstriction, inflammation,
CC	allergies, asthma, impeded respiration, respiratory distress syndrome
CC	(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC	hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC	pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC	and/or cancer. AAAF18434 to AAAF21543 represent human polynucleotide

```
RESULT 10
AA00527/c
ID AA00527 standard; cDNA: 345 BP.
XX
XX AA00527:
XX
XX 02-FEB-1996 (first entry)
XX
XX Human interleukin-15 mature polypeptide.
XX
XX Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..345
XX FT /*tag= a
XX FT /label= corresp. to precursor nts 145-489
XX FT /note= "claimed"
XX
XX MO9527722-A.
XX
XX 19-OCT-1995.
XX
XX 06-APR-1994; 94WO-US03793.
XX
XX 06-APR-1994; 94WO-US03793.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;
XX Rauch C;
XX WPI: 1995-373556/48.
XX P-PSDB: AAR83310.
XX
XX Isolated DNA encoding polypeptide with mammalian IL-15 activity - which
XX stimulates proliferation and differentiation of T cells, used for
XX treating carcinoma(s), melanomas, etc. and viral infections
XX
XX Claim 3; Page 28-29; 48pp; English.
XX
XX A simian species of IL-15 (sIL-15) was purified and its AA
XX sequence and cDNA sequence analysed (see AAR83309, AAR83436,
XX AA00524, AA00525). Both the simian and the human ORFs encode
XX a precursor polypeptide (AAR83436, AAR83438). The precursor
XX polypeptides each comprise a 48-AA leader sequence and a sequence
XX encoding mature simian or human IL-15 polypeptides. The active
XX simian and human IL-15 polypeptides are disclosed in AAR83309 &
XX AAR83310 respectively. The invention also comprises other mammalian
XX IL-15, including human IL-15, that hybridise to probes defined by
XX AAR83438. A plasmid contg. a recombinant clone of human IL-15
XX cDNA was deposited with ATCC on Feb. 19 1993 under ATCC 69245.
XX The deposit was named 141-herf. AAR83435 is a mammalian mature
XX IL-15 polypeptide. It is a generic sequence which encompasses both
XX AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.
XX
XX Sequence 345 BP; 121 A; 49 C; 68 G; 107 T; 0 other;
```

```
Query Match 84.7%; Score 14.4; DB 16; Length 345;
Best Local Similarity 70.6%; Pred. No. 1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 ACRTRCTYTCNGTRTA 17
   11:11:11:11:11:11
DB 92 ACATCACTTCCGTATA 76
```

```
RESULT 11
AAF57024/c
```

```
ID AAF57024 standard; cDNA: 345 BP.
XX
XX AAF57024;
XX
XX 14-MAY-2001 (first entry)
XX
XX Simian ETF (SETF) mature polypeptide encoding cDNA.
XX
XX Epithelium-derived T-cell factor; ETF; simian; human; enteritis;
XX gastrointestinal disease; mucositis; peptic ulcer; cytostatic;
XX villus atrophic disorder; inflammatory bowel disease; antiinflammatory;
XX anti-HIV; antiviral; T-lymphocyte stimulator; ss.
XX
XX Mammalia.
XX
XX Key Location/Qualifiers
XX CDS 1..345
XX FT /*tag= a
XX FT /product= "mature SETF"
XX
XX US6184359-B1.
XX
XX 06-FEB-2001.
XX
XX 09-NOV-1998; 98US-0189193.
XX
XX 22-FEB-1995; 95US-0393305.
XX 04-OCT-1996; 96US-0725969.
XX 08-MAR-1993; 93US-0031399.
XX 22-APR-1994; 94US-0233606.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;
XX
XX WPI: 2001-217801/22.
XX P-PSDB: AAB62013.
XX
XX New antibodies that specifically binds epithelium-derived T-cell factor
XX polypeptide useful for e.g. treating or preventing gastrointestinal
XX diseases, HIV and HIV-associated diseases, augmenting destruction of
XX tumour cells -
XX
XX Disclosure: Fig 1; 35pp; English.
```

```
XX The invention relates to simian and human epithelium-derived T-cell
XX factor (ETF) polypeptides. Antibodies that specifically bind to the ETF
XX polypeptides are used for treating or preventing gastrointestinal
XX diseases, such as chemotherapy and radiation therapy-induced enteritis
XX and mucositis, peptic ulcer disease, villus atrophic disorders and
XX inflammatory bowel disease; for increasing tolerated doses for radiation
XX therapy and chemotherapy agents which are limited by gastrointestinal
XX toxicity; and for treating HIV and HIV-associated diseases. The
XX antibodies are further used to treat a variety of other diseases or
XX conditions where it is desired to stimulate proliferation of
XX T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B
XX lymphocytes, to augment anti-infectious disease immunity, to induce CTL,
XX LAK or NK lytic activity, or to augment the destruction of tumour cells
XX or cells infected with virus. The present sequence represents a cDNA
XX encoding the simian ETF (SETF) mature polypeptide.
```

```
XX Sequence 345 BP; 121 A; 49 C; 68 G; 107 T; 0 other;
```

```
Query Match 84.7%; Score 14.4; DB 22; Length 345;
Best Local Similarity 70.6%; Pred. No. 1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 ACRTRCTYTCNGTRTA 17
   11:11:11:11:11:11
DB 92 ACATCACTTCCGTATA 76
```

RESULT 8

ID AAF57023 standard; DNA; 17 BP.

AC AAF57023;

DT 14-MAY-2001 (first entry)

DE Simian ETF cDNA specific degenerate primer.

KW Epithelium-derived T-cell factor; ETF; simian; human; enteritis;

KW gastrointestinal disease; mucositis; peptic ulcer; cytostatic;

KW villus atrophic disorder; inflammatory bowel disease; antiinflammatory;

KW anti-HIV; antiviral; T-lymphocyte stimulator; PCR primer; ss.

OS Synthetic.

PN US6184359-B1.

PD 06-FEB-2001.

PF 09-NOV-1998; 98US-0189193.

PR 22-FEB-1995; 95US-0393305.

PR 04-OCT-1996; 96US-0725969.

PR 08-MAR-1993; 93US-0031399.

PR 22-APR-1994; 94US-0233606.

PA (IMMV) IMMUNEX CORP.

PI Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;

DR WPI; 2001-217801/22.

XX New antibodies that specifically binds epithelium-derived T-cell factor

XX polypeptide useful for e.g. treating or preventing gastrointestinal

XX diseases, HIV and HIV-associated diseases, augmenting destruction of

XX tumour cells -

XX Example 3; Column 25; 35pp; English.

XX The invention relates to simian and human epithelium-derived T-cell

XX factor (ETF) polypeptides. Antibodies that specifically bind to the ETF

XX polypeptides are used for treating or preventing gastrointestinal

XX diseases, such as chemotherapy and radiation therapy-induced enteritis

XX and mucositis, peptic ulcer disease, villus atrophic disorders and

XX inflammatory bowel disease; for increasing tolerated doses for radiation

XX therapy and chemotherapy agents which are limited by gastrointestinal

XX toxicity; and for treating HIV and HIV-associated diseases. The

XX antibodies are further used to treat a variety of other diseases or

XX conditions where it is desired to stimulate proliferation of

XX T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B

XX lymphocytes, to augment anti-infectious disease immunity, to induce CTL,

XX LAK or NK lytic activity, or to augment the destruction of tumour cells

XX or cells infected with virus. Sequences AAF57021-23 represent PCR primers

XX used for simian ETF (SETF) cDNA cloning.

XX Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

XX Query Match 84.7%; Score 14.4; DB 22; Length 17;

XX Best Local Similarity 100.0%; Pred. No. 71;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTCTCTCTGCTGTTA 17

DB 1 acrtctctctgctgtrta 17

RESULT 9

AAT00525/C

ID AAT00525 standard; cDNA; 345 BP.

AC AAT00525;

DT 02-FEB-1996 (first entry)

DE Simian interleukin-15 mature polypeptide.

KW Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.

KW Cebus apella.

FH Key Location/Qualifiers

FT CDS 1..345

FT /tag= a

FT /label= precursor nts 145-489

FT /note= "Claimed"

PN W09527722-A.

PD 19-OCT-1995.

PF 06-APR-1994; 94WO-US03793.

PR 06-APR-1994; 94WO-US03793.

PA (IMMV) IMMUNEX CORP.

PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;

DR P-PSDB; AAR83309.

XX WPI: 1995-373556/48.

XX Isolated DNA encoding polypeptide with mammalian IL-15 activity - which

XX stimulates proliferation and differentiation of T cells, used for

XX treating carcinoma(s), melanomas, etc. and viral infections

XX Claim 2; Page 26; 48pp; English.

XX A simian species of IL-15 (sIL-15) was purified and analysed by SDS-

XX PAGE. Bioassay of unstained gel slices indicated IL-15 activity was

XX assoc. with proteins having mol. wts in the range of 15-17 kDa. The

XX N-terminus of the 15-17 kDa was sequenced. The results indicated the

XX identity of the first 33 AAs of AAR83309. Subsequent sequencing of a

XX cDNA clone obtd. from a simian library provided a sequence encoding

XX the polypeptide AAR83436. AAR83436 comprises a relatively short 48 AA

XX leader sequence and a mature polypeptide AAR83309. The sequence of the

XX N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers

XX for the amplification of IL-15-specific DNA sequences. The first

XX 6 AAs of the N-terminus were used to design one primer, a

XX degenerate mixture coding for all possible codon usages - AAT00528.

XX The AA sequences of the simian mature N-terminus 26-31 were used

XX to design a second primer, a degenerate mixture coding for a

XX complement of all possible codon usages of AAs 26-31, omitting

XX posn. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA

XX cells were used as templates. A 92 bp DNA fragment was used as a

XX hybridisation probe to screen a portion of a plasmid library contg.

XX cDNA inserts prepd. from CV-1/EBNA polyadenylated RNA. This

XX resulted in the isolation of clone C85.sIL-15 that has an ORF

XX given in AAT00524. AAR83309 is the active polypeptide & AAR83436 is

XX the precursor polypeptide. AAT00525 encodes the active polypeptide.

XX Sequence 345 BP; 124 A; 50 C; 64 G; 107 T; 0 other;

XX Query Match 84.7%; Score 14.4; DB 16; Length 345;

XX Best Local Similarity 70.6%; Pred. No. 1e+02;

XX Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTCTCTCTGCTGTTA 17

DB 92 ACATCACTTCTGTGTTA 76

AA29485
ID AAX29485 standard; DNA: 17 BP.
XX
AC AAX29485;
XX
DT 10-JUN-1999 (first entry)
XX
DE Simian ETF DNA amplifying primer.
XX
KW Epithelium-derived T-cell factor; ETF: immunoassay; enteritis; ulcer;
KW T cell proliferation; gastrointestinal disease; mucositis; colitis;
KW gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease;
KW human immune deficiency virus; tumour; simian; PCR primer; ss.
XX
OS Synthetic.
XX
PN US5892001-A.
XX
PD 06-APR-1999.
XX
PE 04-OCT-1996; 96US-0725969.
XX
PR 22-FEB-1995; 95US-0393305.
PR 08-MAR-1993; 93US-0031399.
PR 22-APR-1994; 94US-0233606.
PR 04-OCT-1996; 96US-0725969.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI Rauch C;
XX
DR WPI: 1999-253930/21.
XX
PT Antibodies specific for epithelium-derived T-cell growth factor
XX
PS Example 3; Columns 25; 34pp; English.
XX
CC The invention relates to an isolated antibody that binds specifically to
CC a simian or human epithelium-derived T-cell factor (ETF) polypeptide.
CC The antibodies are used, optionally when immobilized or labeled, to
CC detect and quantify ETF in standard immunoassays. They may also be used
CC as diagnostic and therapeutic agents, e.g. when conjugated to toxins (or
CC their precursors) or radionuclides. ETF induces proliferation and/or
CC differentiation of T cells (or their precursors), e.g. for use in
CC establishing long term in vitro cultures; and is also used to treat
CC gastrointestinal disease (e.g. enteritis or mucositis induced by
CC chemotherapy or radiation, peptide ulcer, gastroenteritis, colitis,
CC villus atrophy, malignancy and inflammatory bowel disease), to treat
CC human immune deficiency virus infection or associated disease, or
CC generally in any situation requiring stimulation of T or B cell
CC proliferation, secretion of immunoglobulins or certain cytokines,
CC increased anti-infectious disease immunity, induction of T-cell lytic
CC activity or increased destruction of tumour or virus-infected cells.
CC Sequences AAX29483-85 represent primers for PCR amplification of the
CC simian ETF DNA sequences.
XX
SO Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

Query Match 84.7%; Score 14.4; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTRCTYTCNGTRTA 17
DB 1 acrtctctylcngtrta 17

RESULT 7
AA238248
ID AAX238248 standard; DNA: 17 BP.
XX

AA238248;
AC
XX
DT 09-FEB-2000 (first entry)
XX
DE Simian ETF degenerate PCR primer #11.
XX
KW ETF: epithelium-derived T-cell factor; T-cell; T-lymphocyte;
KW proliferation; differentiation; growth factor; precursor; mature; CD4+;
KW CD8+; gastrointestinal; epithelium; cell culture; treatment; HIV;
KW gastrointestinal disease; gastroenteritis; colitis;
KW inflammatory bowel disease; villus atrophic disorder; enteritis;
KW chemotherapy; radiotherapy; gut toxicity; cancer; side effect;
KW tolerated dose; PCR; primer; ss.
XX
OS Synthetic.
XX
PN Mammalia.
XX
PD US5985262-A.
XX
PE 16-NOV-1999.
XX
PR 03-FEB-1997; 97US-0794524.
XX
PR 22-FEB-1995; 95US-0393305.
PR 04-OCT-1996; 96US-0726817.
PR 08-MAR-1993; 93US-0031399.
PR 22-APR-1994; 94US-0233606.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Rauch C, Fung V, Eisenman JR, Grabstein KH, Anderson DM;
PI P-PSDB; AAY52313.
XX
DR WPI: 2000-022267/02.
XX
PT Stimulation of T-cells in human immunodeficiency virus infected
PT patients -
XX
PS Example 3; Column 25; 33pp; English.
XX
CC This sequence represents simian ETF degenerate PCR primer #11,
CC used with degenerate primer #9 (AA238246) to amplify a fragment
CC of the gene encoding simian epithelium-derived T-cell factor (ETF).
CC This was used to probe a simian cDNA library for a clone with a
CC complete open reading frame (AA238224). The primers were based on
CC N-terminal amino acid sequences in the purified ETF protein.
CC ETF is a previously unidentified T-cell growth factor which
CC stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to
CC proliferate and differentiate. It also promotes proliferation of the
CC gastrointestinal epithelium. The protein can be used to promote long-term
CC in vitro culture of T-lymphocytes and T-cell lines. ETF can be used for
CC treating HIV infection, HIV-associated diseases, and other diseases or
CC conditions where stimulation of T-cell proliferation would be desirable
CC e.g., it could be used to augment the destruction of tumour cells or
CC virally-infected cells. ETF may also be used to treat or prevent
CC gastrointestinal disease, including chemotherapy and radiotherapy
CC associated enteritis, gastroenteritis, colitis, inflammatory bowel
CC disease and villus atrophic disorders. Chemotherapy and radiotherapy
CC associated enteritis (gut toxicity) results in bleeding and sepsis due to
CC gastrointestinal flora entering the blood, and thus can limit the dosage
CC of therapeutic agent administered to a cancer patient. ETF may therefore
CC be used to increase the tolerated doses radiotherapy and chemotherapy.
XX
SO Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

Query Match 84.7%; Score 14.4; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTRCTYTCNGTRTA 17
DB 1 acrtctctylcngtrta 17

CC CV1/EBNA cDNA library for the full-length SEF coding sequence.
CC Mature SEF induces proliferation and/or differentiation of precursor
CC or mature T cells and is useful for promoting long-term in vitro
CC culture of T-lymphocytes and T-cell lines. It is used for treating
CC gastrointestinal diseases including peptic ulcer, colitis and
CC malignancy and for treating HIV infection.
XX
SQ Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

Query Match 84.7%; Score 14.4; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTCTCTTCNGTCTTA 17
| | | | | | | | | | | | | | | | | | | | |
Db 1 acrtctcttcngtctta 17

RESULT 4

AAV42246
ID AAV42246 standard; DNA; 17 BP.

XX AAT42246;

XX 05-FEB-1997 (first entry)

XX Simian ETF gene primer #2 based on amino acids 26-31 of mature ETF.

XX Epithelium-derived T-cell factor; simian; human; culture; proliferation;
KW epithelial cell; differentiation; T-lymphocyte; African green monkey;
KW primer; PCR; polymerase chain reaction; amplification; probe; ss.

XX Synthetic.

XX US5552303-A.

XX 03-SEP-1996.

XX 08-MAR-1993; 93US-0031399.

XX 08-MAR-1993; 93US-0031399.

XX (IMMV) IMMUNEX CORP.

XX Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;

XX WPI: 1996-412063/41.

XX New isolated simian and human epithelium-derived T-cell factors -
PT which stimulate the proliferation and/or differentiation of
PT T-lymphocytes and T-cell lines

XX Example 3; Column 17; 22pp; English.

XX Primers AAT42244-6 were used to amplify a 92 bp fragment of the African
CC green monkey epithelium-derived T-cell factor (ETF; AAT42243). The
CC sequence of this primer is based on amino acids 26-31 of the mature ETF
CC protein sequence obtained by peptide sequencing the purified protein.
CC The template for the amplification was cDNA derived from monkey kidney
CC CV-1/EBNA cells stimulated to proliferate by phorbol 12-myristate
CC 13-acetate. The 92 bp fragment was labelled and used as a probe to
CC isolate a clone c85. SEF which contained the simian gene. ETF is a
CC protein of 15-17 kD which is expressed by epithelial cells and
CC stimulates proliferation and/or differentiation of precursor and/or
CC mature T cells. The protein is therefore useful for promoting long term
CC in vivo culture of T-lymphocytes and T-cell lines.

XX Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

Query Match 84.7%; Score 14.4; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 71;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTCTCTTCNGTCTTA 17
| | | | | | | | | | | | | | | | | | | | |
Db 1 acrtctcttcngtctta 17

RESULT 5

AAV02877
ID AAV02877 standard; DNA; 17 BP.

XX AAV02877;

XX 08-MAY-1998 (first entry)

XX Simian epithelium derived T-cell factor PCR primer 3.

XX Epithelium derived T-cell factor; ETF; simian; gastrointestinal disease;
KW B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;
KW treatment; prevention; PCR primer; ss.

XX Synthetic.

XX Simian.

XX US5707616-A.

XX 13-JAN-1998.

XX 04-OCT-1996; 96US-0726817.

XX 22-FEB-1995; 95US-0393305.

XX 08-MAR-1993; 93US-0031399.

XX 22-APR-1994; 94US-0233606.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;

XX Rauch C;

XX WPI: 1998-100295/09.

XX Treatment or prevention of gastrointestinal diseases - by
PT administering epithelium-derived T-cell factor polypeptide
PT

XX Example 3; Column 43-44; 34pp; English.

XX PCR primers AAV02875-V02877 are used in the amplification of a simian
CC epithelium-derived T-cell factor (ETF) which is used in a method for
CC treating or preventing gastrointestinal disease. These polypeptides have
CC particular application in the treatment of gastrointestinal disorders
CC associated with disruption of the gastrointestinal epithelium or villi
CC such as chemotherapy- and radiation-therapy induced enteritis (gut
CC toxicity), mucositis, peptic ulcer disease, gastroenteritis and colitis,
CC villus atrophic disorders, malignancy and inflammatory bowel disease.
CC ETF polypeptides may also be useful in the treatment of human
CC immunodeficiency virus (HIV) and HIV-associated disease due to their
CC ability to stimulate CD4+ and CD8+ cells. Biologically active ETF may be
CC used to treat a variety of other diseases or conditions where T-cell or
CC B-cell stimulation is desired.

XX Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

Query Match 84.7%; Score 14.4; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTCTCTTCNGTCTTA 17
| | | | | | | | | | | | | | | | | | | | |
Db 1 acrtctcttcngtctta 17

RESULT 6

XX DR WPI; 1995-373556/48.
 XX
 PT Isolated DNA encoding polypeptide with mammalian IL-15 activity - which
 PT stimulates proliferation and differentiation of T cells, used for
 PT treating carcinoma(s), melanomas, etc. and viral infections
 XX
 PS Example: Page 21; 48pp; English.
 XX
 CC A simian species of IL-15 (sIL-15) was purified and analysed by SDS-
 CC PAGE. Bioassay of unstained gel slices indicated IL-15 activity was
 CC assoc. with proteins having mol. wts in the range of 15-17 kDa. The
 CC N-terminus of the 15-17 kDa was sequenced. The results indicated the
 CC identity of the first 33 AAs of AAR83309. Subsequent sequencing of a
 CC cDNA clone obtd. from a simian library provided a sequence encoding
 CC the polypeptide AAR83436. AAR83436 comprises a relatively short 48 AA
 CC leader sequence and a mature polypeptide AAR83309. The sequence of the
 CC N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers
 CC for the amplification of IL-15-specific DNA sequences. The first
 CC 6 AAs of the N-terminus were used to design one primer, a
 CC degenerate mixture coding for all possible codon usages - AAT00528.
 CC The AA sequences of the simian mature N-terminus 26-31 were used
 CC to design a second primer, a degenerate mixture coding for a
 CC complement of all possible codon usages of AAs 26-31, omitting
 CC post. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA
 CC cells were used as templates. A 92 bp DNA fragment was used as a
 CC hybridisn. probe to screen a portion of a plasmid library contg.
 CC cDNA inserts prep. from CV-1/EBNA polyadenylated RNA. This
 CC resulted in the isolation of clone C85. sIL-15 that has an ORF
 CC given in AAT00524. AAR83309 is the active polypeptide & AAR83436 is
 CC the precursor polypeptide.
 XX
 SQ Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

Query Match 84.7%; Score 14.4; DB 16; Length 17;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTCRCYTCNGTRFA 17
 ||||||||||||||||
 Db 1 acrtcrctcngtrta 17

RESULT 2
 AA084587
 ID AA084587 standard; cDNA; 17 BP.
 XX
 AC AA084587;
 XX
 DT 04-SEP-1995 (first entry)
 XX
 DE Simian IL-15 primer.
 XX
 KW Interleukin-15; IL-15; sIL-15; T-cell growth factor;
 KW African green monkey; CV-1; antitumor; virucide; primer; PCR;
 KW polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 PN ZA9402636-A.
 XX
 PD 28-DEC-1994.
 XX
 PF 18-APR-1994; 94ZA-0002636.
 XX
 PR 18-APR-1994; 94ZA-0002636.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 PI Rauch C;

DR WPI; 1995-082473/11.
 XX
 PT New purified interleukin-15 - which induces T cell proliferation
 PT and differentiation, used for the treatment of tumours and viral
 PT infection
 XX
 PS Example 3; Page 21; 47pp; English.
 XX
 CC cDNA generated from PMA-stimulated CV-1/EBNA cells was amplified
 CC by PCR using primers (AA084585-87) based on the N-terminal sequence
 CC of simian interleukin-15 (sIL-15). A clone encoding sIL-15 was
 CC obtained (AA084583).
 XX
 SQ Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

Query Match 84.7%; Score 14.4; DB 16; Length 17;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTCRCYTCNGTRFA 17
 ||||||||||||||||
 Db 1 acrtcrctcngtrta 17

RESULT 3
 AAT94959
 ID AAT94959 standard; cDNA; 17 BP.
 XX
 AC AAT94959;
 XX
 DT 11-MAR-1997 (first entry)
 XX
 DE Epithelium derived T cell factor PCR primer.
 XX
 KW Simian epithelium derived T cell factor; sETF; African green monkey;
 KW Cercopithecus aethiops; CV1/EBNA cell; T-cell; B-cell; lymphocyte;
 KW proliferation; differentiation; gastrointestinal; HIV infection;
 KW human immunodeficiency virus; polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 PN US5574138-A.
 XX
 PD 12-NOV-1996.
 XX
 PR 08-MAR-1993; 93US-0031399.
 XX
 PR 22-FEB-1995; 95US-0393305.
 XX
 PR 08-MAR-1993; 93US-0031399.
 XX
 PR 22-APR-1994; 94US-0233606.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 PI Rauch C;
 XX
 DR WPI; 1996-517923/51.
 XX
 PT New epithelium derived T cell factor - induces proliferation of T
 PT and B cells, stimulates destruction of tumour and virus-infected
 PT cells and protects against toxicity, partic. for treating intestinal
 PT disease and HIV infection
 XX
 PS Example 3; Column 25; 35pp; English.
 XX
 CC The simian ETF (epithelium derived T cell factor) was isolated from
 CC African green monkey CV1/EBNA cell conditioned medium. The N-
 CC terminal sequence of the purified sETF was determined and then PCR
 CC primers were designed based on the sequence information. The
 CC present sequence is that of a degenerate primer based on amino acids
 CC 26-31, i.e. Tyr-Thr-Glu-Ser-Asp-Val. A 92 bp fragment was
 CC amplified from CV1/EBNA DNA and was used as a probe to screen a

BASE COUNT 146 a 75 c 87 g 145 t
ORIGIN

Query Match 84.7%; Score 14.4; DB 9; Length 453;
Best Local Similarity 70.6%; Pred. No. 7.1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTGCTCTGNGTRTA 17
||:||||:||||:|
Db 202 ACATCACTTCCGTATA 186

Search completed: June 19, 2002, 02:54:34
Job time: 7092 sec

ORIGIN

Query Match 84.7%; Score 14.4; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACRTCTCTTCNGTCTATA 17
Db 1 ACRTCTCTTCNGTCTATA 17

RESULT 7
LOCUS AR070288 345 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 12 from patent US 5892001.
ACCESSION AR070288
VERSION AR070288.1 GI:7221176
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 345)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Epithelium-derived T-cell factor antibodies
JOURNAL Patent: US 5892001-A 12 06-APR-1999;
FEATURES Location/Qualifiers
source 1..345

BASE COUNT 121 a 49 c 68 g 107 t
ORIGIN

Query Match 84.7%; Score 14.4; DB 6; Length 345;
Best Local Similarity 70.6%; Pred. No. 7.1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACRTCTCTTCNGTCTATA 17
Db 92 ACATCCTTTCCTGATA 76

RESULT 8
LOCUS AR070289 345 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 13 from patent US 5892001.
ACCESSION AR070289
VERSION AR070289.1 GI:7221177
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 345)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Epithelium-derived T-cell factor antibodies
JOURNAL Patent: US 5892001-A 13 06-APR-1999;
FEATURES Location/Qualifiers
source 1..345

BASE COUNT 124 a 50 c 64 g 107 t
ORIGIN

Query Match 84.7%; Score 14.4; DB 6; Length 345;
Best Local Similarity 70.6%; Pred. No. 7.1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACRTCTCTTCNGTCTATA 17
Db 92 ACATCCTTTCCTGATA 76

RESULT 9

AR085747/c 345 bp DNA linear PAT 07-SEP-2000
LOCUS AR085747
DEFINITION Sequence 12 from patent US 5985262.
ACCESSION AR085747
VERSION AR085747.1 GI:10012513
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 345)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Method of treatment with epithelium derived T-cell factor
JOURNAL Patent: US 5985262-A 12 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..345

BASE COUNT 121 a 49 c 68 g 107 t
ORIGIN

Query Match 84.7%; Score 14.4; DB 6; Length 345;
Best Local Similarity 70.6%; Pred. No. 7.1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACRTCTCTTCNGTCTATA 17
Db 92 ACATCCTTTCCTGATA 76

RESULT 10
LOCUS AR085748 345 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 13 from patent US 5985262.
ACCESSION AR085748
VERSION AR085748.1 GI:10012514
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 345)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Method of treatment with epithelium derived T-cell factor
JOURNAL Patent: US 5985262-A 13 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..345

BASE COUNT 124 a 50 c 64 g 107 t
ORIGIN

Query Match 84.7%; Score 14.4; DB 6; Length 345;
Best Local Similarity 70.6%; Pred. No. 7.1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACRTCTCTTCNGTCTATA 17
Db 92 ACATCCTTTCCTGATA 76

RESULT 11
LOCUS I28856 345 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 12 from patent US 5574138.
ACCESSION I28856
VERSION I28856.1 GI:1819640
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 345)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Epithelium-derived T-cell factor
JOURNAL Patent: US 5574138-A 12 12-NOV-1996;

Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACRTCRCTYCNGTRTA 17
|||||
Db 1 ACRTCRCTYCNGTRTA 17

RESULT 2
AR070287 17 bp DNA linear PAT 18-FEB-2000
LOCUS Sequence 11 from patent US 5892001.
DEFINITION AR070287
ACCESSION AR070287
VERSION AR070287.1 GI:7221175
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Epithelium-derived T-cell factor antibodies
JOURNAL Patent: US 5892001-A 11 06-Apr-1999;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 2 a /organism="unknown"
ORIGIN 4 c 1 g 5 t 5 others

Query Match 84.7%; Score 14.4; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACRTCRCTYCNGTRTA 17
|||||
Db 1 ACRTCRCTYCNGTRTA 17

RESULT 3
AR085746 17 bp DNA linear PAT 07-SEP-2000
LOCUS Sequence 11 from patent US 5985262.
DEFINITION AR085746
ACCESSION AR085746
VERSION AR085746.1 GI:10012512
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Method of treatment with epithelium derived T-cell factor
JOURNAL Patent: US 5985262-A 11 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 2 a /organism="unknown"
ORIGIN 4 c 1 g 5 t 5 others

Query Match 84.7%; Score 14.4; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACRTCRCTYCNGTRTA 17
|||||
Db 1 ACRTCRCTYCNGTRTA 17

RESULT 4
I25788 17 bp DNA linear PAT 07-OCT-1996
LOCUS Sequence 11 from patent US 5552303.
DEFINITION I25788
ACCESSION I25788
VERSION I25788.1 GI:1605658

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE DNA encoding epithelium-derived T-cell factor
JOURNAL Patent: US 5552303-A 11 03-SEP-1996;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 2 a /organism="unknown"
ORIGIN 4 c 1 g 5 t 5 others

Query Match 84.7%; Score 14.4; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACRTCRCTYCNGTRTA 17
|||||
Db 1 ACRTCRCTYCNGTRTA 17

RESULT 5
I28855 17 bp DNA linear PAT 06-FEB-1997
LOCUS Sequence 11 from patent US 5574138.
DEFINITION I28855
ACCESSION I28855
VERSION I28855.1 GI:1819638
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Epithelium-derived T-cell factor
JOURNAL Patent: US 5574138-A 11 12-NOV-1996;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 2 a /organism="unknown"
ORIGIN 4 c 1 g 5 t 5 others

Query Match 84.7%; Score 14.4; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACRTCRCTYCNGTRTA 17
|||||
Db 1 ACRTCRCTYCNGTRTA 17

RESULT 6
I79225 17 bp DNA linear PAT 10-JUN-1998
LOCUS Sequence 11 from patent US 5707616.
DEFINITION I79225
ACCESSION I79225
VERSION I79225.1 GI:3207515
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Method for treating or preventing gastrointestinal disease with
epithelium-derived T-cell factor
JOURNAL Patent: US 5707616-A 11 13-JAN-1998;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 2 a /organism="unknown"
ORIGIN 4 c 1 g 5 t 5 others

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 02:54:34 ; Search time 1924.67 Seconds
(without alignments)
184.837 Million cell updates/sec

Title: US-09-724-841-11

Perfect score: 17

Sequence: 1 ACRTCRCTTCNGTRTA 17

Scoring table: IDENTITY_NUC

Gapop 10.0 , Capext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb.ba:*

2: gb.htg:*

3: gb.in:*

4: gb.om:*

5: gb.ov:*

6: gb.pat:*

7: gb.ph:*

8: gb.pl:*

9: gb.pr:*

10: gb.ro:*

11: gb.sts:*

12: gb.sy:*

13: gb.un:*

14: gb.vl:*

15: em.ba:*

16: em.fun:*

17: em.hum:*

18: em.in:*

19: em.mu:*

20: em.om:*

21: em.or:*

22: em.ov:*

23: em.pat:*

24: em.ph:*

25: em.pl:*

26: em.ro:*

27: em.sts:*

28: em.un:*

29: em.vl:*

30: em.htg.hum:*

31: em.htg.liv:*

32: em.htg.other:*

33: em.htgo.liv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

1	14.4	84.7	17	6	AR004273	AR004273 Sequence
2	14.4	84.7	17	6	AR070287	AR070287 Sequence
3	14.4	84.7	17	6	AR085746	AR085746 Sequence
4	14.4	84.7	17	6	125788	125788 Sequence 11
5	14.4	84.7	17	6	128855	128855 Sequence 11
6	14.4	84.7	17	6	179225	179225 Sequence 11
7	14.4	84.7	345	6	AR070288	AR070288 Sequence
8	14.4	84.7	345	6	AR070289	AR070289 Sequence
9	14.4	84.7	345	6	AR085747	AR085747 Sequence
10	14.4	84.7	345	6	AR085748	AR085748 Sequence
11	14.4	84.7	345	6	128856	128856 Sequence 12
12	14.4	84.7	345	6	128857	128857 Sequence 13
13	14.4	84.7	345	6	179226	179226 Sequence 12
14	14.4	84.7	345	6	179227	179227 Sequence 13
15	14.4	84.7	453	9	HSIL15MR	238000 H.sapiens m
16	14.4	84.7	486	9	HSIL15	Y09908 H.sapiens m
17	14.4	84.7	489	4	AF108148	AF108148 Felis cat
18	14.4	84.7	489	6	AR004267	AR004267 Sequence
19	14.4	84.7	489	6	AR004268	AR004268 Sequence
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21	14.4	84.7	489	6	AR024349	AR024349 Sequence
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24	14.4	84.7	489	6	AR085740	AR085740 Sequence
25	14.4	84.7	489	6	AR085741	AR085741 Sequence
26	14.4	84.7	489	6	AR094649	AR094649 Sequence
27	14.4	84.7	489	6	AR094650	AR094650 Sequence
28	14.4	84.7	489	6	AR122045	AR122045 Sequence
29	14.4	84.7	489	6	AR122046	AR122046 Sequence
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31	14.4	84.7	489	6	AR122868	AR122868 Sequence
32	14.4	84.7	489	6	AR125104	AR125104 Sequence
33	14.4	84.7	489	6	AR125105	AR125105 Sequence
34	14.4	84.7	489	6	AX006785	AX006785 Sequence
35	14.4	84.7	489	6	AX006786	AX006786 Sequence
36	14.4	84.7	489	6	AX320242	AX320242 Sequence
37	14.4	84.7	489	6	AX320244	AX320244 Sequence
38	14.4	84.7	489	6	BD008811	BD008811 Antagonis
39	14.4	84.7	489	6	BD008812	BD008812 Antagonis
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41	14.4	84.7	489	6	125783	125783 Sequence 4
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43	14.4	84.7	489	6	128850	128850 Sequence 4
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ALIGNMENTS

RESULT 1

AR004273

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

BASE COUNT

ORIGIN

Sequence 11 from patent US 5747024.

AR004273

GI:3965152

Unknown.

Unknown.

Unclassified.

1 (bases 1 to 17)

Grabsstein,K.H. and Widmer,M.B.

Vaccine adjuvant comprising Interleukin-15

Patent: US 5747024-A 11 05-MAY-1998;

Location/Qualifiers

1..17

/organism="unknown"

2 a

4 c

1 g

5 t

5 others

Query Match

Best Local Similarity

84.7%: Score 14.4; DB 6; Length 17;

100.0%: Pred. No. 7.6e+02;

Wed Jun 19 09:13:58 2002

us-09-724-841-10.rn1

Page 7

Search completed: June 19, 2002, 02:22:12
Job time: 5420 sec

OY 1 ACRTGNGAYTCNGTRTA 17
DB 1043 ACATCTGACTCTGTGTA 1027

RESULT 10

US-08-307-896-6/c
Sequence 6, Application US/08307896C
Patent No. 6034071
GENERAL INFORMATION:
APPLICANT: Iyengar, Sriivas Ravi
TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL
FILE REFERENCE: 29770
CURRENT APPLICATION NUMBER: US/08/307,896C
CURRENT FILING DATE: 1994-09-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 2092
TYPE: DNA
ORGANISM: Homo sapiens
US-08-307-896-6

Query Match 81.2%; Score 13.8; DB 3; Length 2092;
Best Local Similarity 70.6%; Pred. No. 25;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGNGAYTCNGTRTA 17
DB 869 ACCTCGATTCTGTATA 853

RESULT 11

PCT-US95-11808-6/c
Sequence 6, Application PC/TUS9511808
GENERAL INFORMATION:
APPLICANT: Iyengar, Sriivas Ravi V.
TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND
TITLE OF INVENTION: ADENYLYL
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue and
ADDRESS: Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11808
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,896
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Richard S.
REGISTRATION NUMBER: 26,154
REFERENCE/DOCKET NUMBER: 29970 165/28755
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEFAX: (212) 765-2519
TELEX: 650 611063
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 2092 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..2092
OTHER INFORMATION: /product= "adenylyl cyclase
OTHER INFORMATION: 2
OTHER INFORMATION: (partial)"
PCT-US95-11808-6

Query Match 81.2%; Score 13.8; DB 5; Length 2092;
Best Local Similarity 70.6%; Pred. No. 25;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGNGAYTCNGTRTA 17
DB 869 ACCTCGATTCTGTATA 853

RESULT 12

US-08-307-896-5/c
Sequence 5, Application US/08307896C
Patent No. 6034071
GENERAL INFORMATION:
APPLICANT: Iyengar, Sriivas Ravi
TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL
TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
FILE REFERENCE: 29770
CURRENT APPLICATION NUMBER: US/08/307,896C
CURRENT FILING DATE: 1994-09-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 4008
TYPE: DNA
ORGANISM: Rattus norvegicus
US-08-307-896-5

Query Match 81.2%; Score 13.8; DB 3; Length 4008;
Best Local Similarity 70.6%; Pred. No. 27;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGNGAYTCNGTRTA 17
DB 2780 ACATCTGACTCTGTGTA 2764

RESULT 13

US-08-726-214-3/c
Sequence 3, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Yang, Wei-Jen
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,193
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-189-193-10

Query Match 81.2%; Score 13.8; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGAYTCNGTRTA 17
DB 1 ACRTGAYTCNGTRTA 17

RESULT 8
PCT-US94-03793-10
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eismann, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: Interleukin-15
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03793
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lauer, Charlene
REGISTRATION NUMBER: 33,035

REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
PCT-US94-03793-10

Query Match 81.2%; Score 13.8; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGAYTCNGTRTA 17
DB 1 ACRTGAYTCNGTRTA 17

RESULT 9
US-08-726-214-17/c
Sequence 17, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1652 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-726-214-17

Query Match 81.2%; Score 13.8; DB 3; Length 1652;
Best Local Similarity 70.6%; Pred. No. 24;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHEICAL: NO
ANTI-SENSE: YES
US-08-504-042-10

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Best Local Similarity 100.0%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGNGAYTCNGTTRTA 17
Db 1 ACRTGNGAYTCNGTTRTA 17

RESULT 5
US-08-725-969-10
Sequence 10, Application US/08725969
Patent No. 5892001
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,969
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-725-969-10

Query Match 81.2%; Score 13.8; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGNGAYTCNGTTRTA 17
Db 1 ACRTGNGAYTCNGTTRTA 17

RESULT 6
US-08-794-524-10
Sequence 10, Application US/08794524
Patent No. 5985262
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,524
FILING DATE: 03-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-794-524-10

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Best Local Similarity 100.0%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACRTGNGAYTCNGTTRTA 17

RESULT 7
US-09-189-193-10
Sequence 10, Application US/09189193
Patent No. 6184359
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15

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Db      1 ACRTGNGAYTCNGTRTA 17

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RESULT 2
 US-08-393-305-10
 : Sequence 10, Application US/08393305
 : Patent No. 5574138
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Grabstein, Kenneth
 :
 : APPLICANT: Anderson, Dirk
 :
 : APPLICANT: Eisenman, June
 :
 : APPLICANT: Fung, Victor
 :
 : APPLICANT: Rauch, Charles
 :
 : TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
 :
 : NUMBER OF SEQUENCES: 15
 :

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1  SOFTWARE: PatentIn Release #1.0, Version #1.25
2
3  CURRENT APPLICATION DATA:
4  APPLICATION NUMBER: US/08/3953,305
5  FILING DATE: 22-FEB-1995
6
7  CLASSIFICATION: 424
8
9  ATTORNEY/AGENT INFORMATION:
10 NAME: Mcmasters, David D.
11 REGISTRATION NUMBER: 33,963
12 REFERENCE/DOCKET NUMBER: 480052.409C2
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: 206-622-4900
15 INFORMATION FOR SEQ ID NO: 10:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 17 base pairs
18 TYPE: nucleic acid
19 STRANDEDNESS: single
20 TOPOLOGY: linear
21
22 US-08-393-305-10

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RESULT 3
 US-08-726-817-10
 ; Sequence 10, Application US/08726817
 ; Patent No. 5707616
 ; GENERAL INFORMATION:
 ; APPLICANT: Grabstein, Kenneth
 ; APPLICANT: Anderson, Dirk
 ; APPLICANT: Eisenman, June
 ; APPLICANT: Fung, Victor
 ; APPLICANT: Rauch, Charles
 ; TITLE OF INVENTION: EPITHELUM-DERIVED T-CELL FACTOR
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle

```

STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,817
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-726-817-10

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Query Match	81.2%	Score 13.8	DB 1	Length 17
Best Local Similarity	100.0%	Pred. No. 14		
Matches 17, Conservative	0	Mismatches	0	Gaps 0

RESULT 4
 : US-08-504-042-10
 : Sequence 10, Application US/08504042
 : Patent No. 5747024
 : GENERAL INFORMATION:
 : APPLICANT: Grabstejn, Kenneth
 : APPLICANT: Anderson, Dirk
 : APPLICANT: Eismann, June
 : APPLICANT: Fung, Victor
 : APPLICANT: Rauch, Charles
 : TITLE OF INVENTION: Epithelium-derived T-cell Factor
 : NUMBER OF SEQUENCES: 12
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: Immunex Corporation
 : STREET: 51 University Street
 : CITY: Seattle
 : STATE: Washington
 : COUNTRY: USA
 : ZIP: 98101
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/504,042
 : FILING DATE: 19-JUL-1995
 : CLASSIFICATION: 424
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/031,399
 : FILING DATE: 08-MAR-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Lanner, Charlene
 : REGISTRATION NUMBER: 33,035

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 02:22:11 ; Search time 66.01 seconds
(without alignments)
63.260 Million cell updates/sec

Title: US-09-724-841-10

Perfect score: 17

Sequence: 1 ACRTGNGAYTCNGTRTA 17

Scoring table: IDENTITY_NUC

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Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: /cgn2_6/prodata/2/1na/6B.COMB.seq:*
5: /cgn2_6/prodata/2/1na/FCIUS.COMB.seq:*
6: /cgn2_6/prodata/2/1na/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	13.8	81.2	17	1	US-08-726-817-10
4	13.8	81.2	17	1	US-08-504-042-10
5	13.8	81.2	17	2	US-08-725-969-10
6	13.8	81.2	17	2	US-08-794-524-10
7	13.8	81.2	17	4	US-09-189-193-10
8	13.8	81.2	17	5	PCT-US94-03793-10
9	13.8	81.2	1652	3	US-08-726-214-17
10	13.8	81.2	2092	3	US-08-307-896-6
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18	12.2	71.8	1327	1	US-08-507-431-3
19	12.2	71.8	1327	2	US-08-700-546-1
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22	12.2	71.8	1327	4	US-09-219-277-3
23	12.2	71.8	1327	4	US-09-599-661-3
24	12.2	71.8	4291	2	US-08-417-210A-81
25	12.2	71.8	5199	3	US-08-726-214-13
26	12.2	71.8	17710	4	US-08-976-259-70
27	11.8	69.4	115	1	US-07-920-281C-4

C	28	11.8	69.4	115	4	US-08-466-277-4	Sequence 4, Appl
	29	11.8	69.4	1449	4	US-08-858-207A-68	Sequence 68, Appl
	30	11.8	69.4	1876	2	US-08-466-589-7	Sequence 7, Appl
	31	11.8	69.4	1876	3	US-08-700-636-7	Sequence 7, Appl
	32	11.8	69.4	1876	3	US-08-467-574-7	Sequence 7, Appl
	33	11.8	69.4	1876	4	US-09-217-345-7	Sequence 7, Appl
	34	11.8	69.4	1929	1	US-07-841-646-26	Sequence 26, Appl
	35	11.8	69.4	1929	5	PCT-US91-07633-3	Sequence 3, Appl
	36	11.8	69.4	2208	5	PCT-US95-08493-1	Sequence 1, Appl
	37	11.8	69.4	2336	4	US-08-796-101-47	Sequence 47, Appl
	38	11.8	69.4	2580	5	PCT-US95-08493-18	Sequence 18, Appl
	39	11.8	69.4	2604	5	PCT-US95-08493-20	Sequence 20, Appl
	40	11.8	69.4	2610	1	US-08-374-834-17	Sequence 17, Appl
	41	11.8	69.4	2610	1	US-08-644-271-28	Sequence 28, Appl
	42	11.8	69.4	2869	1	US-08-374-834-2	Sequence 2, Appl
	43	11.8	69.4	2869	1	US-08-644-271-2	Sequence 2, Appl
	44	11.8	69.4	3398	5	PCT-US95-08493-12	Sequence 12, Appl
	45	11.8	69.4	3872	2	US-08-331-081B-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-031-399-10
Sequence 10, Application US/08031399
Patent No. 5552303
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: Epithelium-derived T-cell factor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,399
FILING DATE: 19930308
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Launer, Charlene
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-031-399-10

Query Match 81.2%; Score 13.8; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

COMMENT

Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic
sequence.

Job time: 7366 sec

FEATURES

Location/Qualifiers
1..583
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_1ib="cosmid 103j15"
/clone="103j15a5"

BASE COUNT 135 a 122 c 134 g 184 t 8 others
ORIGIN

Query Match 81.2%; Score 13.8; DB 12; Length 583;
Best Local Similarity 70.6%; Pred. No. 1.6e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTGAGATTCGCTGA 17
11:11 11:11 11:11
Db 406 ACCTCAGATTCGGTGA 390

RESULT 15
FR0039660/c 597 bp DNA linear GSS 22-OCT-1999

LOCUS Fugu rubripes GSS sequence, clone 103j15a64, genomic survey
DEFINITION sequence.

ACCESSION AL127155
VERSION 1.1
KEYWORDS GSS; genome survey sequence.

SOURCE Takifugu rubripes.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
1 (bases 1 to 597)

REFERENCE Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K.,
Umaria,Y., Williams,G. and Brenner,S.
Direct Submission

TITLE

Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource
Centre, Hinxton, Cambridge, CB10 1SB. UK Email:

JOURNAL

COMMENT

biohelp@hmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS

DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic
sequence.

FEATURES

Location/Qualifiers
1..597
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_1ib="cosmid 103j15"
/clone="103j15a64"

BASE COUNT 138 a 129 c 136 g 176 t 18 others
ORIGIN

Query Match 81.2%; Score 13.8; DB 12; Length 597;
Best Local Similarity 70.6%; Pred. No. 1.6e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTGAGATTCGCTGA 17
11:11 11:11 11:11
Db 405 ACCTCAGATTCGGTGA 389

Search completed: June 19, 2002, 02:15:53

RESULT 12
AA034789/c
LOCUS
DEFINITION
AA034789 556 bp mRNA linear EST 23-AUG-1996
m153605.r1 Soares mouse embryo NbmEL3.5 14.5 Mus musculus cDNA
clone IMAGE:467241.5' similar to gb:U1993 ADENYLATE CYCLASE, TYPE
II (HUMAN); gb:U12919 Mus musculus adenyllyl cyclase type VII mRNA,
complete (MOUSE); mRNA sequence.

ACCESSION
AA034789
VERSION
AA034789.1 GI:1506671
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 556)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisler,S., Kucaba,T., Lacey,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMIT Mouse EST Project
Unpublished (1996)
JOURNAL
Contact: Maria M/Mouse EST Project
WashU-HMIT Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:281057
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 411.
Location/Qualifiers
1..556
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="467241"
/clone_lib="Soares mouse embryo NBMEL3.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACCAATCTGAAGTGGAGCGCGCGAATTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 1; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
p7733 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Petina Bonaldo."

BASE COUNT 146 a 131 c 146 g 133 t
ORIGIN

Query Match 81.2%; Score 13.8; DB 9; Length 556;
Best Local Similarity 70.6%; Pred. No. 1.6e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTCNGAYTCNGTCTA 17
||:||||:||||:||||:
Db 298 ACATCTGACTCGGTCTA 282

RESULT 13
BI341029/c
LOCUS
BI341029 573 bp mRNA linear EST 30-JUL-2001

DEFINITION
368222 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION
BI341029
VERSION
BI341029.1 GI:15034318
KEYWORDS
EST.
SOURCE
pig.
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE
1 (bases 1 to 573)
Stoene,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keeler,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
JOURNAL
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTACGACG
Plate: 107 row: N column: 5
Seq primer: ATTTCAGTACATCTATAG.
Location/Qualifiers
1..573
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT 140 a 152 c 161 g 119 t 1 others
ORIGIN

Query Match 81.2%; Score 13.8; DB 10; Length 573;
Best Local Similarity 70.6%; Pred. No. 1.6e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTCNGAYTCNGTCTA 17
||:||||:||||:||||:
Db 138 ACGTCTGATTCGTCTA 122

RESULT 14
FR0039639/c
LOCUS
DEFINITION
FR0039639 583 bp DNA linear GSS 22-OCT-1999
Fugu rubripes GSS sequence, clone 103J15aE5, genomic survey
sequence.
ACCESSION
AL127134.1 GI:6108749
VERSION
AL127134
KEYWORDS
GSS: genome survey sequence.
SOURCE
Takifugu rubripes.
ORGANISM
Takifugu rubripes.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
1 (bases 1 to 583)
REFERENCE
Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K.,
Umrania,Y., Williams,G. and Brenner,S.
Direct Submission
Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource
Centre, Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hmp.mrc.ac.uk

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.lnl.gov

Plate: L1AM8441 row: c column: 16

High quality sequence stop: 500.

Location/Qualifiers

1. .502

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3455175"

/clone_lib="NIH_MGC_12"

/tissue_type="cervical carcinoma cell line"

/lab_host="DH10B"

/note="Organ: Cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.4 kb. Library prepared by Life

Technologies."

BASE COUNT 144 a 73 c 87 g 198 t

ORIGIN

Query Match

Best Local Similarity 70.6%; Score 13.8; DB 10; Length 502;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGCAVTCNGTRTA 17

Db 33 ACATCGATTCTGTATA 49

RESULT 10
FR0039629 518 bp DNA linear GSS 22-OCT-1999

LOCUS Fugu rubripes GSS sequence, clone 103J15aF1, genomic survey

DEFINITION sequence.

AL127124

AL127124.1 GI:6108739

GSS: genome survey sequence.

KEYWORDS Takifugu rubripes

SOURCE Takifugu rubripes

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;

Tetraodontidae; Takifugu.

1 (bases 1 to 518)

Elgar, G., Clark, M.S., Smith, S., Meek, S., Warner, S., Edwards, Y.J.K.,

Umanita, Y., Williams, G. and Brenner, S.

Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource

Centre, Hinxton, Cambridge, CB10 1SR. UK Email:

biohelp@hmp.mrc.ac.uk

Vector: pBluescript II KS

V_type: phagemid

PRIMER: KS

DESCR: One pass dye-terminator sequencing of cosmid cloned genomic

sequence.

Location/Qualifiers

1. .518

/organism="Takifugu rubripes"

/db_xref="taxon:31033"

/clone_lib="cosmid 103J15"

/clone="103J15aF1"

BASE COUNT 148 a 122 c 116 g 126 t 6 others

ORIGIN

Query Match

Best Local Similarity 70.6%; Score 13.8; DB 12; Length 518;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGCAVTCNGTRTA 17

Db 11:11 11:11 11:11

DB 415 ACCTCAGATTCGGTGA 431

RESULT 11

AW766896

LOCUS

DEFINITION

AW766896 528 bp mRNA linear EST 16-FEB-2001

da6d11.y1 Harland stage 19-23 Xenopus laevis cDNA clone

IMAGE:3199413 5' similar to TR:097754 097754 TITIN ;, mRNA

sequence.

AW766896.1 GI:7698968

EST.

African clawed frog.

Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 528)

Clifton, S., Johnson, S.L., Blumberg, B., Song, D., Hillier, L., Pape, D.

, Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person

, B., Gibbons, M., Harvey, N., Rittler, E., Jackson, Y., McCann, R.,

Waterston, R. and Wilson, R. 1999

Unpublished (1999)

Contact: Sandy Clifton, Ph.D.

Washu Xenopus EST project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Library constructed by R. Harland, PhD (University of California,

Berkeley)

DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available

through the I.M.A.G.E. Consortium/LINL at:

image.lnl.gov/image/html/resources.shtml

Seq primer: -40RP from GIBCO

High quality sequence stop: 489.

Location/Qualifiers

1. .528

/organism="Xenopus laevis"

/db_xref="taxon:8355"

/clone="IMAGE:3199413"

/clone_lib="Harland stage 19-23"

/tissue_type="neural"

/dev_stage="stage 19-23"

/lab_host="DH10B (phage-resistant)"

/note="Vector: pCS107 (custom); Site_1: NotI; Site_2: SalI

; cDNA made by oligo-dT priming. Library constructed by

Dr. Francesca Mariani in the laboratory of R. Harland,

Ph.D. (University of California, Berkeley). References:

XB-F.2 is a transcriptional repressor that converts

ectoderm into neural tissue. Mariani, F.V. Harland, R.M.,

Development. 1998 Dec;125(24):5019-31. PMID: 9811566; UI:

99030283; Use of large-scale expression cloning screens in

the xenopus laevis tadpole to identify gene function.

Gramer TC, Liu KJ, Mariani FV, Harland RM., Dev Biol.

2000 Dec 15;228(2):197-210. PMID: 1112324; UI: 20564075;

Note: This is a Xenopus Gene Collection (XGC) library."

BASE COUNT 188 a 100 c 114 g 125 t 1 others

ORIGIN

Query Match

Best Local Similarity 70.6%; Score 13.8; DB 9; Length 528;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGCAVTCNGTRTA 17

Db 108 ACATCAGATTCGGTGA 124

KEYWORDS EST,
African clawed frog.

SOURCE Xenopus laevis

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.

REFERENCE 1 (bases 1 to 472)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Haller,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Thakasing,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.

AUTHORS WASHU Xenopus EST project, 1999

JOURNAL Unpublished (1999)

COMMENT Contact: Sandy Clifton, Ph.D.
WASHU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by Bento Soares and M. Fatima Bonaldo (University of Iowa). DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 450.

FEATURES Location/Qualifiers

source 1..472

 /organism="Xenopus laevis"

 /db_xref="taxon:8355"

 /clone="IMAGE:4783632"

 /clone_lib="Blackshear/Soares normalized Xenopus egg library"

 /sex="female"

 /tissue_type="unfertilized egg"

 /cell_type="unfertilized egg"

 /dev_stage="unfertilized egg"

 /lab_host="DH10B"

 /note="Vector: pT73-Pac; Site.1: EcoRI; Site.2: NotI; POLYA-selected mRNA was prepared from unfertilized Xenopus laevis eggs. The library was constructed in the vector pT73-Pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. 'Normalization and subtraction: two approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-dT18 primer: double stranded cDNAs were ligated to EcoRI adapters, digested with NotI, and directionally cloned into the NotI and EcoRI-digested pT73-Pac vector. The library contained approximately 7.2 x 10⁵ recombinants, with average insert sizes of 1-1.5 kb."

BASE COUNT 109 a 110 c 135 g 118 t

ORIGIN

Query Match 81.2%; Score 13.8; DB 10; Length 472;
Best Local Similarity 70.6%; Pred. No. 1.5e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTCGATTCGCTGTA 17
11:11 11:11 11:11

DB 162 ACATCGATTCGCTGTA 146

RESULT 8

LOCUS AI380969 478 bp mRNA linear EST 30-MAR-1999

DEFINITION tg18d12.x1 NCI-CCAP-CL11 Homo sapiens cDNA clone IMAGE:2109143 3', mRNA sequence.

ACCESSION AI380969

VERSION AI380969.1 GI:4190822

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 478)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. consortium/LLNL at: www.bio.llnl.gov/dbip/image/image.html
Insert length: 444 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 466.

FEATURES Location/Qualifiers

source 1..478

 /organism="Homo sapiens"

 /db_xref="taxon:9606"

 /clone="IMAGE:2109143"

 /clone_lib="NCI-CCAP-CL11"

 /tissue_type="B-cell, chronic lymphocytic leukemia"

 /lab_host="DH10B"

 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTCACATCGAGTGGAGCGGCGCCATGCGTCTTTTCTTTTCTTTT T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 146 a 102 c 80 g 149 t 1 others

ORIGIN

Query Match 81.2%; Score 13.8; DB 9; Length 478;
Best Local Similarity 70.6%; Pred. No. 1.5e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTCGATTCGCTGTA 17
11:11 11:11 11:11

DB 106 ACCTCGATTCGCTGTA 122

RESULT 9

LOCUS BE543117 502 bp mRNA linear EST 09-AUG-2000

DEFINITION 601069058F1 NIH-MGC_12 Homo sapiens cDNA clone IMAGE:3455175 5', mRNA sequence.

ACCESSION BE543117

VERSION BE543117.1 GI:97711762

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 502)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.

FEATURES	Location/Qualifiers
SOURCE	1..416
	/organism="Xenopus laevis"
	/db_xref="taxon:8355"
	/clone="XL042d11"
	/clone_1lb="NIBB Mochl normalized Xenopus neurula library"
	/tissue_type="whole embryo"
	/dev_stage="stage 15"
BASE COUNT	91 a 96 c 128 g 100 t 1 others
ORIGIN	
Query Match	81.2%; Score 13.8; DB 10; Length 416;
Best Local Similarity	70.6%; Pred. No. 1.4e+03;
Matches 12: Conservative	3; Mismatches 2; Indels 0; Gaps 0;
OY	1 ACRTCGAYTCNGTETA 17
Db	125 ACATCTGATCTGTGTA 109
RESULT	5
B53166	419 bp DNA linear GSS 20-JUN-1998
LOCUS	CIT-HSP-2009B4.TF CIT-HSP Homo sapiens genomic clone 2009B4, DNA
DEFINITION	sequence.
ACCESSION	B53166
VERSION	B53166.1 GI:2607500
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 419)
AUTHORS	Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden
	,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M.
	and Venter,J.C.
TITLE	Use of a random BAC End Sequence Database for Sequence-Ready Map
	Building
JOURNAL	Unpublished (1997)
COMMENT	Other_GSSs: CIT-HSP-2009B4.TF
	Contact: Mark Adams
	Department of Eukaryotic Genomics
	The Institute for Genomic Research
	9712 Medical Center Dr., Rockville, MD 20850, USA
	Tel: 301 838 0200
	Fax: 301 838 0208
	Email: mdadams@tigr.org
	Clones are available from Research Genetics (Inforesgen.com). BAC
	end search page:
	http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
	Seq primer: M13 Reverse
	Class: BAC ends.
FEATURES	Location/Qualifiers
SOURCE	1..419
	/organism="Homo sapiens"
	/db_xref="GDB:7040670"
	/db_xref="taxon:9606"
	/clone="2009B4"
	/clone_1lb="CIT-HSP"
	/sex="Male"
	/cell_type="Sperm"
	/note="Vector: pBeloBAC11; site_1: HindIII; site_2:
	HindIII"
BASE COUNT	134 a 50 c 65 g 170 t
ORIGIN	
Query Match	81.2%; Score 13.8; DB 12; Length 419;
Best Local Similarity	70.6%; Pred. No. 1.4e+03;
Matches 12: Conservative	3; Mismatches 2; Indels 0; Gaps 0;

QY	1	ACRTGCAVTCNGTRTA	17	
Db	205	ACATCGATTCTGTATA	221	
RESULT	6			
LOCUS	BG017447/c			
DEFINITION	BG017447	470 bp	mRNA	linear
	de6b12.x1 Kirschner embryo Sc10 14	Xenopus laevis	cDNA clone	IMAGE:516263 3' similar to SW:SRB7_HUMAN Q13503 RNA POLYMERASE II HOLOENZYME COMPONENT SRB7 ;, mRNA sequence.
ACCESSION	BG017447			
VERSION	EST			
KEYWORDS	EST			
SOURCE	African clawed frog.			
ORGANISM	Xenopus laevis			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae; Xenopodine; Xenopus.			
REFERENCE	1 (bases 1 to 470)			
AUTHORS	Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.			
	Washu Xenopus EST project, 1999			
TITLE	Unpublished (1999)			
JOURNAL	Contact: Sandy Clifton, Ph.D.			
COMMENT	Washu Xenopus EST project, 1999			
	Washington University School of Medicine			
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA			
	Tel: 314 286 1800			
	Fax: 314 286 1810			
	Email: est@wustl.edu			
	Library constructed by M. Kirschner (Harvard Medical School). DNA Sequencing by: Washington University Genome Sequencing Center			
	Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LNL at: info@image.llnl.gov			
	Seq primer: -40UP from Gldco			
	High quality sequence stop: 315.			
FEATURES	Location/Qualifiers			
source	1..470			
	/organism="Xenopus laevis"			
	/db_xref="taxon:8355"			
	/clone_image="3516263"			
	/clone_id="Kirschner embryo Sc10 14"			
	/tissue_type="Pooled embryos (stage 10-14)"			
	/lab_host="DH10B (phage-resistant)"			
	/note="Vector: pCS2+; Site.1: NotI; Site.2: SalI;			
	Size-selected for average insert size 1.2 kb. Library was constructed and donated by M. Kirschner (Harvard Medical School)."			
BASE COUNT	110 a	95 c	130 g	135 t
ORIGIN				
	Query Match	81.2%	Score 13.8:	DB 10; Length 470;
	Best Local Similarity	70.6%;	Pred. No. 1.5e+03;	
	Matches 12; Conservative	3;	Mismatches 2;	Indels 0;
			Gaps 0;	
QY	1	ACRTGCAVTCNGTRTA	17	
Db	166	ACATCGATTCTGTATA	150	
RESULT	7			
LOCUS	BM191868	472 bp	mRNA	linear
DEFINITION	dag37f01.x3 Blackshear/Soares normalized Xenopus egg library			
	Xenopus laevis cDNA clone IMAGE:4783632 3' similar to SW:SRB7_HUMAN			
	Q13503 RNA POLYMERASE II HOLOENZYME COMPONENT SRB7 ;, mRNA			
	sequence.			
ACCESSION	BM191868			
VERSION	BM191868.1	GI:17527831		

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 02:15:49 ; Search time 2591.91 Seconds
(without alignments)
88.525 Million cell updates/sec

Title: us-09-724-841-10

Perfect score: 17

Sequence: 1 ACRTGNGATYTCNGTTRIA 17

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estcov:*
6: em_estipl:*
7: em_estro:*
8: em_nlc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.8	81.2	301	9	AW788294 C00336-F
2	13.8	81.2	352	9	AV705097 AV705097
3	13.8	81.2	405	10	BF887255 CM4-TN014
4	13.8	81.2	416	10	BJ052660 BJ052660
5	13.8	81.2	419	12	B53166 CIT-HSP-200
6	13.8	81.2	470	10	BC017447 de64b12.x
7	13.8	81.2	472	10	BM191868 dag37f01.
8	13.8	81.2	478	9	AI380969 tg18d12.x
9	13.8	81.2	502	10	BE543117 6010690058
10	13.8	81.2	518	12	AL127124 Fugu rubr
11	13.8	81.2	528	9	AW766896 da61d11.y
12	13.8	81.2	556	9	AA034789 m153d05.x
13	13.8	81.2	573	10	BI341029 368222 MA
14	13.8	81.2	583	12	AL127134 Fugu rubr
15	13.8	81.2	597	12	FR0039639 Fugu rubr
16	13.8	81.2	599	12	AL127150 Fugu rubr
17	13.8	81.2	609	12	FR0039649 AL127144 Fugu rubr

C 18	13.8	81.2	643	10	W98391	W98391 mg20a05.r1
C 19	13.8	81.2	726	10	BC306142	BC306142 fm52g08.x
C 20	13.8	81.2	738	12	AI184518	A2184518 SP-1003-A
C 21	13.8	81.2	750	12	BH327893	BH327893 CH230-124
C 22	13.8	81.2	789	10	BC823603	BC823603 602728993
C 23	13.8	81.2	848	9	AI322582	AI322582 m153d05.y
C 24	13.8	81.2	863	9	AU119404	AU119404 AU119404
C 25	13.8	81.2	962	12	CNS01XNS	AL171937 Tetradon
C 26	13.8	81.2	1036	12	CNS050RX	AL149638 Tetradon
C 27	13.8	81.2	1547	12	AG031697	AG031697 Pan tlog1
C 28	12.8	75.3	153	10	BG609709	BG609709 323656 MA
C 29	12.8	75.3	212	9	BB348982	BB348982 BB348982
C 30	12.8	75.3	215	10	BG450224	BG450224 NF015E10D
C 31	12.8	75.3	219	9	AA035435	AA035435 zk25f11.r
C 32	12.8	75.3	220	10	BE350988	BE350988 ht22b05.x
C 33	12.8	75.3	234	9	AA716548	AA716548 z970c04.s
C 34	12.8	75.3	234	10	BE827388	BE827388 CM2-ET001
C 35	12.8	75.3	235	12	BH354835	BH354835 CH230-331
C 36	12.8	75.3	247	9	AW312889	AW312889 5259 MARC
C 37	12.8	75.3	253	12	BH185768	BH185768 028.M.03-
C 38	12.8	75.3	253	12	CNS070EJ	AL1622717 t3 end of
C 39	12.8	75.3	259	10	Z21283	Z21283 HSNADMXU T
C 40	12.8	75.3	260	9	AV266760	AV266760 AV266760
C 41	12.8	75.3	262	10	BM071779	BM071779 fu87911.x
C 42	12.8	75.3	263	10	BE846090	BE846090 232309 BA
C 43	12.8	75.3	264	9	BI119275	BI119275 BI119275
C 44	12.8	75.3	265	10	BI438396	BI438396 1c22608.Y
C 45	12.8	75.3	276	9	AV143032	AV143032 AV143032

ALIGNMENTS

RESULT 1	AW788294	301 bp	linear	EST 01-MAY-2001
LOCUS	C00336-F	Lambda Zap, StrataGene	Blumeria graminis f. sp. hordei	
DEFINITION	CDNA clone C00336, mRNA sequence.			
ACCESSION	AW788294			
VERSION	AW788294.1	GI:13899891		
KEYWORDS	EST.			
SOURCE	Blumeria graminis f. sp. hordei.			
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Erysiphales; Erysiphaceae; Blumeria.			
REFERENCE	1 (bases 1 to 301)			
AUTHORS	Thomas,S.W., Rasmussen,S.W., Glaring,M.A., Rouster,J.A. and Oliver			
TITLE	Gene identification in the fungal pathogen Blumeria graminis by expressed sequence tag analysis			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Rasmussen,S.W. Department of Yeast Genetics Carlsberg Laboratory 10 GI. Carlsbergvej, DK-2500, Copenhagen, Denmark Tel: 45 3327 5230 Fax: 45 3327 4766 Email: svre@erc.dk High quality sequence stop: 301 POLYA-NO.			
FEATURES	Location/Qualifiers			
source	1..301			
	/organism="Blumeria graminis f. sp. hordei"			
	/db_xref="taxon:62688"			
	/clone="C00336"			
	/clone_id="Lambda Zap, StrataGene"			
	/cell_type="condia"			
	/lab_host="Hordeum vulgare"			
BASE COUNT	94 a 72 c 59 g 75 t			
ORIGIN	1 others			
Query Match	81.2%; Score 13.8; DB 9; Length 301;			

DE Streptococcus pneumoniae pbp1A TER isolate g) nucleotide sequence.
 XX
 KW Streptococcus pneumoniae; penicillin binding protein; pbp2B; pbp1A;
 KM transpeptidase encoding region; TER; antibiotic resistance; diagnosis;
 XX detection; identification; pneumococcal meningitis; ss.
 OS Streptococcus pneumoniae.
 XX
 PN ZA9807024-A.
 PD 28-APR-1999.
 XX
 PF 05-AUG-1998; 982A-0007024.
 PR 01-AUG-1997; 972A-0006886.
 XX
 PA (SAME-) SOUTH AFRICAN INST MEDICAL RES.
 PA (UYWI-) UNIV WITWATERSRAND.
 PA (MEDI-) MEDICAL RES COUNCIL.
 PI Klugman KP, Smith AM, Du Plessis M;
 PI WPI; 1999-601770/51.
 DR
 XX
 PT Polymerase chain reaction assays for detecting Streptococcus pneumonia
 PT useful for the diagnosis of pneumococcal meningitis
 XX
 PS Claim 11; Fig 4; 63pp; English.
 XX
 CC A polymerase chain reaction (PCR) assays have been developed for
 CC detecting an antibiotic resistant strain of Streptococcus pneumoniae
 CC using primers based on the penicillin binding protein 2B (pbp2B) gene
 CC and the pbp1A gene. The products and methods can be used for detecting
 CC S. pneumoniae, particularly antibiotic-resistant strains. They can be
 CC used for simultaneously diagnosing pneumococcal meningitis and
 CC identifying any antibiotic-resistant S. pneumoniae strains in a sample.
 CC The methods can be used for detecting S. pneumoniae strains resistant
 CC to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin.
 CC The assays can be adapted to detect other pathogens causing meningitis.
 CC S. pneumoniae with a minimum inhibitory concentration (MIC) of
 CC 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and
 CC a 224 bp product. The present sequence represents a Streptococcus
 CC pneumoniae pbp1A transpeptidase encoding region (TER) isolate nucleotide
 CC sequence from the present invention.
 XX
 SQ Sequence 1260 BP; 404 A; 281 C; 268 G; 307 T; 0 other;
 Query Match 81.2%; Score 13.8; DB 20; Length 1260;
 Best Local Similarity 70.6%; Pred. No. 1.3e+02;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 1 ACRTGCAATCNGTRTA 17
 DB 903 ACGTCCGATTCGCTATA 887
 RESULT 15
 AAZ35946/C
 ID AAZ35946 standard; DNA; 1260 BP.
 XX
 AC AAZ35946;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Streptococcus pneumoniae pbp1A TER isolate h) nucleotide sequence.
 XX
 KW Streptococcus pneumoniae; penicillin binding protein; pbp2B; pbp1A;
 KM transpeptidase encoding region; TER; antibiotic resistance; diagnosis;
 XX detection; identification; pneumococcal meningitis; ss.
 OS Streptococcus pneumoniae.

XX
 PN ZA9807024-A.
 XX
 PD 28-APR-1999.
 XX
 PF 05-AUG-1998; 982A-0007024.
 PR 01-AUG-1997; 972A-0006886.
 XX
 PA (SAME-) SOUTH AFRICAN INST MEDICAL RES.
 PA (UYWI-) UNIV WITWATERSRAND.
 PA (MEDI-) MEDICAL RES COUNCIL.
 PI Klugman KP, Smith AM, Du Plessis M;
 PI WPI; 1999-601770/51.
 DR
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 PT useful for the diagnosis of pneumococcal meningitis
 XX
 PS Claim 11; Fig 4; 63pp; English.
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 CC detecting an antibiotic resistant strain of Streptococcus pneumoniae
 CC using primers based on the penicillin binding protein 2B (pbp2B) gene
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 CC S. pneumoniae, particularly antibiotic-resistant strains. They can be
 CC used for simultaneously diagnosing pneumococcal meningitis and
 CC identifying any antibiotic-resistant S. pneumoniae strains in a sample.
 CC The methods can be used for detecting S. pneumoniae strains resistant
 CC to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin.
 CC The assays can be adapted to detect other pathogens causing meningitis.
 CC S. pneumoniae with a minimum inhibitory concentration (MIC) of
 CC 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and
 CC a 224 bp product. The present sequence represents a Streptococcus
 CC pneumoniae pbp1A transpeptidase encoding region (TER) isolate nucleotide
 CC sequence from the present invention.
 XX
 SQ Sequence 1260 BP; 406 A; 284 C; 267 G; 303 T; 0 other;
 Query Match 81.2%; Score 13.8; DB 20; Length 1260;
 Best Local Similarity 70.6%; Pred. No. 1.3e+02;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 1 ACRTGCAATCNGTRTA 17
 DB 903 ACGTCCGATTCGCTATA 887
 Search completed: June 19, 2002, 02:20:52
 Job time: 5410 sec

OY 1 ACRTGCAATTCNGTRTA 17
 DB 717 ACCTCCGATTCGGTATA 701

RESULT 12
 AA235943/C
 ID AA235943 standard; DNA: 1260 BP.

AC AA235943;

DT 07-FEB-2000 (first entry)

DE Streptococcus pneumoniae pbp1A TER isolate e) nucleotide sequence.

KW Streptococcus pneumoniae; penicillin binding protein: pbp2B; pbp1A;

KM transpeptidase encoding region; TER; antibiotic resistance; diagnosis;

XX detection; identification; pneumococcal meningitis; ss.

OS Streptococcus pneumoniae.

PN ZA9807024-A.

PD 28-APR-1999.

PF 05-AUG-1998; 982A-0007024.

PR 01-AUG-1997; 972A-0006886.

PA (SAME-) SOUTH AFRICAN INST MEDICAL RES.

PI (UYWI-) UNIV WITWATERSRAND.

PI (MEDI-) MEDICAL RES COUNCIL.

PI Klugman KP, Smith AM, Du Plessis M;

PI WPI; 1999-601770/51.

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PS useful for the diagnosis of pneumococcal meningitis

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CC detecting an antibiotic resistant strain of Streptococcus pneumoniae

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CC and the pbp1A gene. The products and methods can be used for detecting

CC S. pneumoniae, particularly antibiotic-resistant strains. They can be

CC used for simultaneously diagnosing pneumococcal meningitis and

CC identifying any antibiotic-resistant S. pneumoniae strains in a sample.

CC The methods can be used for detecting S. pneumoniae strains resistant

CC to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin.

CC The assays can be adapted to detect other pathogens causing meningitis.

CC S. pneumoniae with a minimum inhibitory concentration (MIC) of

CC 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and

CC a 224 bp product. The present sequence represents a Streptococcus

CC pneumoniae pbp1A transpeptidase encoding region (TER) isolate nucleotide

CC sequence from the present invention.

XX Sequence 1260 BP; 408 A; 286 C; 263 G; 303 T; 0 other;

XX Query Match 81.2%; Score 13.8; DB 20; Length 1260;

XX Best Local Similarity 70.6%; Pred. NO. 1.3e+02;

XX Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGCAATTCNGTRTA 17

DB 903 ACCTCCGATTCGGTATA 887

RESULT 13

AA235944/C
 ID AA235944 standard; DNA: 1260 BP.

AC AA235944;

DT 07-FEB-2000 (first entry)

DE Streptococcus pneumoniae pbp1A TER isolate f) nucleotide sequence.

KW Streptococcus pneumoniae; penicillin binding protein: pbp2B; pbp1A;

KM transpeptidase encoding region; TER; antibiotic resistance; diagnosis;

XX detection; identification; pneumococcal meningitis; ss.

OS Streptococcus pneumoniae.

PN ZA9807024-A.

PD 28-APR-1999.

PF 05-AUG-1998; 982A-0007024.

PR 01-AUG-1997; 972A-0006886.

PA (SAME-) SOUTH AFRICAN INST MEDICAL RES.

PI (UYWI-) UNIV WITWATERSRAND.

PI (MEDI-) MEDICAL RES COUNCIL.

PI Klugman KP, Smith AM, Du Plessis M;

PI WPI; 1999-601770/51.

PT Polymerase chain reaction assays for detecting Streptococcus pneumonia

PS useful for the diagnosis of pneumococcal meningitis

XX Claim 11; Fig 4; 63pp; English.

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CC detecting an antibiotic resistant strain of Streptococcus pneumoniae

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CC and the pbp1A gene. The products and methods can be used for detecting

CC S. pneumoniae, particularly antibiotic-resistant strains. They can be

CC used for simultaneously diagnosing pneumococcal meningitis and

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CC The methods can be used for detecting S. pneumoniae strains resistant

CC to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin.

CC The assays can be adapted to detect other pathogens causing meningitis.

CC S. pneumoniae with a minimum inhibitory concentration (MIC) of

CC 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and

CC a 224 bp product. The present sequence represents a Streptococcus

CC pneumoniae pbp1A transpeptidase encoding region (TER) isolate nucleotide

CC sequence from the present invention.

XX Sequence 1260 BP; 403 A; 291 C; 267 G; 299 T; 0 other;

XX Query Match 81.2%; Score 13.8; DB 20; Length 1260;

XX Best Local Similarity 70.6%; Pred. NO. 1.3e+02;

XX Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGCAATTCNGTRTA 17

DB 903 ACCTCCGATTCGGTATA 887

RESULT 14

AA235945/C

ID AA235945 standard; DNA: 1260 BP.

AC AA235945;

DT 07-FEB-2000 (first entry)

XX AAC98828;
 AC AH01023/c
 DT AAH01023 standard; DNA; 1199 BP.
 XX
 DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:56.
 KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
 KW detection; diagnosis; identification; cytotoxic; neuroprotective;
 KW neoplastic; immunomodulatory; relaxant; contraceptive; gynaecological;
 KW antiinflammatory; cardiact; gene therapy; chromosome mapping;
 KW linkage analysis; tissue identification; tissue typing; forensic;
 KW neural; immune system; muscular; reproductive; gastrointestinal;
 KW pulmonary; cardiovascular; renal; proliferative; ss.
 XX Homo sapiens.
 OS
 PN MO20005320-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US05989.
 XX
 PR 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2000-579444/54.
 DR P-PSDB; AAB54063.
 XX
 PT New nucleic acid that is a pancreatic cancer antigen for preventing,
 PT treating, or ameliorating a medical condition, particular pancreatic
 PT cancer, or for use in assays for diagnosing a pathological condition -
 XX
 XX Claim 1; Page 535; 1379pp; English.
 PS
 CC AAC98773 to AAC99231 encode the human pancreatic cancer associated
 CC proteins, called pancreatic cancer antigens, given in AAB54008 to
 CC AAB54466. The human pancreatic cancer antigens have cytostatic,
 CC neuroprotective, neoplastic, immunomodulatory, relaxant, contraceptive,
 CC gynaecological, cardiact and antiinflammatory activities, and can be used
 CC in gene therapy. The polynucleotide and proteins can be used for
 CC preventing, treating, or ameliorating a medical condition or in assays
 CC for diagnosing a pathological condition or a susceptibility to one in a
 CC subject. Binding partners to the proteins and the activity of the
 CC proteins can be identified. The pancreatic cancer antigens can be used to
 CC detect, treat or prevent pancreatic disorders, especially cancer.
 CC Agonists and antagonists to the antigens can be screened for. The
 CC pancreatic cancer antigen polynucleotides can be used to design nucleic
 CC acid hybridisation probes that can be used in chromosome mapping, linkage
 CC analysis, tissue identification and/or typing in a variety of forensic
 CC and diagnostic methods. The proteins can be used to generate antibodies
 CC which are used to purify, detect and target the polypeptides, including
 CC both in vivo and in vitro diagnostic and therapeutic methods. The
 CC proteins can be used to treat or prevent neural, immune system, muscular,
 CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
 CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
 CC sequences used in the exemplification of the present invention.
 CC
 XX Sequence 1140 BP; 297 A; 271 C; 293 G; 275 T; 4 other;
 SO

Query Match 81.2%; Score 13.8; DB 21; Length 1140;
 Best Local Similarity 70.6%; Pred. No. 1.3e+02;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRICNGAYTNGRTTA 17
 11:11 11:11 11:11
 DB 534 ACGTCGATCTGTATA 518

RESULT 11
 ID AAH01023/c
 XX AAH01023 standard; DNA; 1199 BP.
 AC
 XX AAH01023;
 DT 24-JUL-2001 (first entry)
 XX
 DE Streptococcus pneumoniae nucleotide sequence SEQ ID NO:1014.
 KW Streptococcus pneumoniae; pneumonia; pneumonia; pneumonia;
 KW identification; algal; archaeal; bacterial; fungal; parasitical;
 KW microorganism; diagnosis; translation elongation factor Tu; toxin;
 KW translation elongation factor G; RecA recombinase; resistance;
 KW catalytic subunit of proton-translocating ATPase; antimicrobial;
 KW vaccine; primer; ds.
 XX
 OS Streptococcus pneumoniae.
 XX
 PN MO200123604-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000WO-CA01150.
 XX
 PR 28-SEP-1999; 99CA-2283458.
 XX
 PR 19-MAR-2000; 2000CA-2307010.
 XX
 PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
 XX
 PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M,
 PI Picard FJ, Roy PH;
 XX
 DR WPI; 2001-245006/25.
 XX
 PT Nucleic acid sequences are used to generate universal probes and
 PT primers which can be used to identify and detect the presence of algal,
 PT archaeal, bacterial, fungal and parasitical species in a test sample -
 XX
 XX Claim 27; Page 968; 1580pp; English.
 PS
 CC The present invention describes a method for generating a repository of
 CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
 CC and/or primers are derived. The method comprises amplifying the nucleic
 CC acids of determined algal, archaeal, bacterial, fungal and parasitical
 CC species with a combination of defined primer pairs. The method can be
 CC used for producing probes and/or primers for detecting one or more
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 CC parasites, for universal detection and for specific and ubiquitous
 CC detection and identification of an algal, archaeal, bacterial, fungal
 CC and parasitical species, genus, family and group. A nucleic acid (I)
 CC obtained using the method of the invention can be used for the universal
 CC detection of any bacterium, fungus or parasite in a sample and for the
 CC detection of at least one antimicrobial agent resistance gene or at
 CC least one toxin gene. hexa nucleic acids are used for the specific and
 CC ubiquitous detection and for identification of Streptococcus pneumoniae.
 CC (I) can be used to design a therapeutic agent which is effective against
 CC microorganisms. Microbial species or genus or family or phylum or group
 CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
 CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
 CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp.,
 CC Neisseria gonorrhoeae and Staphylococcus sp. Using DNA based tests
 CC provides faster results than substrate specificity tests as results can
 CC be determined in an hour and improved accuracy is also achieved.
 CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
 CC which are given in the exemplification of the present invention.
 CC
 XX Sequence 1199 BP; 386 A; 286 C; 240 G; 287 T; 0 other;
 SO

Query Match 81.2%; Score 13.8; DB 22; Length 1199;
 Best Local Similarity 70.6%; Pred. No. 1.3e+02;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 8

AAFS7022
ID AAF57022 standard; DNA; 17 BP.

XX AAF57022;

DT 14-MAY-2001 (first entry)

DE Simian ETF cDNA specific degenerate primer.

XX Epithelium-derived T-cell factor; ETF; simian; human; enteritis;

XX gastrointestinal disease; mucositis; peptic ulcer; cytostatic;

XX Villus atrophy disorder; inflammatory bowel disease; antiinflammatory;

XX anti-HIV; antiviral; T-lymphocyte stimulator; PCR primer; ss.

XX Synthetic.

XX US6184359-B1.

XX 06-FEB-2001.

XX 09-NOV-1998; 98US-0189193.

XX 22-FEB-1995; 95US-0393305.

XX 04-OCT-1996; 96US-0725969.

XX 08-MAR-1993; 93US-0031399.

XX 22-APR-1994; 94US-0233606.

XX (IMV) IMMUNEX CORP.

XX Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;

XX WPI; 2001-217801/22.

XX New antibodies that specifically binds epithelium-derived T-cell factor

XX polypeptide useful for e.g. treating or preventing gastrointestinal

XX diseases, HIV and HIV-associated diseases, augmenting destruction of

XX tumour cells

XX Example 3; Column 25; 35pp; English.

XX The invention relates to simian and human epithelium-derived T-cell

XX factor (ETF) polypeptides. Antibodies that specifically bind to the ETF

XX polypeptides are used for treating or preventing gastrointestinal

XX diseases, such as chemotherapy and radiation therapy-induced enteritis

XX and mucositis, peptic ulcer disease, villus atrophic disorders and

XX inflammatory bowel disease; for increasing tolerated doses for radiation

XX therapy and chemotherapy agents which are limited by gastrointestinal

XX toxicity; and for treating HIV and HIV-associated diseases. The

XX antibodies are further used to treat a variety of other diseases or

XX conditions where it is desired to stimulate proliferation of

XX T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B

XX lymphocytes, to augment anti-infectious disease immunity, to induce CTL,

XX LAK or NK lytic activity, or to augment the destruction of tumour cells

XX or cells infected with virus. Sequences AAF57021-23 represent PCR primers

XX used for simian ETF (ETF) cDNA cloning.

XX Sequence 17 BP; 3 A; 3 C; 2 G; 4 T; 5 other;

XX Query Match 81.2%; Score 13.8; DB 22; Length 17;

XX Best Local Similarity 100.0%; Pred. No. 83;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGCAATCNGTCTA 17

DB 1 acrtgcaatcngtctita 17

RESULT 9

AAS65068/c

ID AAS65068 standard; CDNA; 631 BP.

XX AAS65068;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #872.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX P-PADB; ABG00881.

XX New isolated polynucleotide and encoded polypeptides, useful in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits and to assess

XX biodiversity

XX Claim 1; SEQ ID No 872; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

XX polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX and gene mapping, and in recombinant production of (II). The

XX polynucleotides are also used in diagnostics as expressed sequence tags

XX for identifying expressed genes. (I) is useful in gene therapy techniques

XX to restore normal activity of (II) or to treat disease states involving

XX a food supplement. (II) and its binding partners are useful in medical

XX imaging of sites expressing (II). (I) and (II) are useful for treating

XX disorders involving aberrant protein expression or biological activity.

XX the polypeptide and polynucleotide sequences have applications in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits to assess biodiversity

XX and to produce other types of data and products dependent on DNA and

XX amino acid sequences. AAS64197-AAS94564 represent novel human

XX diagnostic coding sequences of the invention.

XX Note: The sequence data for this patent did not appear in the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 631 BP; 99 A; 196 C; 158 G; 178 T; 0 other;

XX Query Match 81.2%; Score 13.8; DB 23; Length 631;

XX Best Local Similarity 70.6%; Pred. No. 1,2e+02;

XX Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGCAATCNGTCTA 17

DB 234 ACRTGCAATCNGTCTA 218

RESULT 10

AAC98828/c

ID AAC98828 standard; CDNA; 1140 BP.

AAZ38247; standard; DNA; 17 BP.
 AAX29484; standard; DNA; 17 BP.
 AAX29484; standard; DNA; 17 BP.
 10-JUN-1999 (first entry)
 Simian ETF DNA amplifying primer.
 Epithelium-derived T-cell factor; ETF; immunoassay; enteritis; ulcer;
 T cell proliferation; gastrointestinal disease; mucositis; colitis;
 gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease;
 human immune deficiency virus; tumour; simian; PCR primer; ss.
 Synthetic.
 US5892001-A.
 06-APR-1999.
 04-OCT-1996; 96US-0725969.
 22-FEB-1995; 95US-0393305.
 08-MAR-1993; 93US-0031399.
 22-APR-1994; 94US-0233606.
 04-OCT-1996; 96US-0725969.
 (IMNV) IMMUNEX CORP.
 Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 Rauch C;
 WPI: 1999-253930/21.
 Antibodies specific for epithelium-derived T-cell growth factor
 Example 3; Columns 25; 34pp; English.
 The invention relates to an isolated antibody that binds specifically to
 a simian or human epithelium-derived T-cell factor (ETF) polypeptide.
 The antibodies are used, optionally when immobilized or labeled, to
 detect and quantify ETF in standard immunoassays. They may also be used
 as diagnostic and therapeutic agents, e.g. when conjugated to toxins (or
 their precursors) or radionuclides. ETF induces proliferation and/or
 differentiation of T cells (or their precursors), e.g. for use in
 establishing long term in vitro cultures; and is also used to treat
 gastrointestinal disease (e.g. enteritis or mucositis induced by
 chemotherapy or radiation, peptide ulcer, gastroenteritis, colitis,
 villus atrophy, malignancy and inflammatory bowel disease), to treat
 human immune deficiency virus infection or associated disease, or
 generally in any situation requiring stimulation of T or B cell
 proliferation, secretion of immunoglobulins or certain cytokines,
 increased anti-infectious disease immunity, induction of T-cell lytic
 activity or increased destruction of tumour or virus-infected cells.
 Sequences AAX29483-85 represent primers for PCR amplification of the
 simian ETF DNA sequences.
 Sequence 17 BP; 3 A; 3 C; 2 G; 4 T; 5 other;
 Query Match 81.2%; Score 13.8; DB 20; Length 17;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 ACRTGCGATGCTGTA 17
 ||||||||||||||||
 1 actcngaytcngtrta 17
 RESULT 7
 AAZ38247 standard; DNA; 17 BP.
 ID AAX38247 standard; DNA; 17 BP.
 XX

AAZ38247; standard; DNA; 17 BP.
 AAX29484; standard; DNA; 17 BP.
 AAX29484; standard; DNA; 17 BP.
 09-FEB-2000 (first entry)
 Simian ETF degenerate PCR primer #10.
 ETF; epithelium-derived T-cell factor; T-cell; T-lymphocyte;
 proliferation; differentiation; growth factor; precursor; mature; CD4+;
 CD8+; gastrointestinal; epithelium; cell culture; treatment; HIV;
 gastrointestinal disease; gastroenteritis; colitis;
 inflammatory bowel disease; villus atrophic disorder; enteritis;
 chemotherapy; radiotherapy; gut toxicity; cancer; side effect;
 tolerated dose; PCR; primer; ss.
 Synthetic.
 Mammalia.
 US5985262-A.
 16-NOV-1999.
 03-FEB-1997; 97US-0794524.
 22-FEB-1995; 95US-0393305.
 04-OCT-1996; 96US-0726817.
 08-MAR-1993; 93US-0031399.
 22-APR-1994; 94US-0233606.
 (IMNV) IMMUNEX CORP.
 Rauch C, Fung V, Eisenman JR, Grabstein KH, Anderson DM;
 PI: 2000-022267/02.
 WPI: 2000-022267/02.
 P-PSDB: AAY52313.
 Stimulation of T-cells in human immunodeficiency virus infected
 patients -
 Example 3; Column 25; 33pp; English.
 This sequence represents simian ETF degenerate PCR primer #10,
 used with degenerate primer #9 (AAZ38246) to amplify a fragment
 of the gene encoding simian epithelium-derived T-cell factor (ETF).
 This was used to probe a simian cDNA library for a clone with a
 complete open reading frame (AAZ38224). The primers were based on
 N-terminal amino acid sequences in the purified ETF protein.
 ETF is a previously unidentified T-cell growth factor which
 stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to
 proliferate and differentiate. It also promotes proliferation of the
 gastrointestinal epithelium. The protein can be used to promote long-term
 in vitro culture of T-lymphocytes and T-cell lines. ETF can be used for
 treating HIV infection, HIV-associated diseases, and other diseases or
 conditions where stimulation of T-cell proliferation would be desirable
 e.g., it could be used to augment the destruction of tumour cells or
 vitally-infected cells. ETF may also be used to treat or prevent
 gastrointestinal disease, including chemotherapy and radiotherapy
 associated enteritis, gastroenteritis, colitis, inflammatory bowel
 disease and villus atrophic disorders. Chemotherapy and radiotherapy
 associated enteritis (gut toxicity) results in bleeding and sepsis due to
 gastrointestinal flora entering the blood, and thus can limit the dosage
 of therapeutic agent administered to a cancer patient. ETF may therefore
 be used to increase the tolerated doses radiotherapy and chemotherapy.
 Sequence 17 BP; 3 A; 3 C; 2 G; 4 T; 5 other;
 Query Match 81.2%; Score 13.8; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 ACRTGCGATGCTGTA 17
 ||||||||||||||||
 1 actcngaytcngtrta 17

CC CVI/EBNA cDNA library for the full-length SEF coding sequence.
 CC Mature SEF induces proliferation and/or differentiation of precursor
 CC or mature T cells and is useful for promoting long-term in vitro
 CC culture of T-lymphocytes and T-cell lines. It is used for treating
 CC gastrointestinal diseases including peptic ulcer, colitis and
 CC malignancy and for treating HIV infection.

XX Sequence 17 BP: 3 A; 3 C; 2 G; 4 T; 5 other;

Query Match 81.2%; Score 13.8; DB 17; Length 17;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGCAATCNGTCTTA 17
 |||||||
 DB 1 acrtcngaytcngtrta 17

RESULT 4

AAAT42245
 ID AAT42245 standard; DNA: 17 BP.

AC AAT42245;

DT 05-FEB-1997 (first entry)

DE Simian ETF gene primer #1 based on amino acids 26-31 of mature ETF.

XX Epithelium-derived T-cell factor; simian; human; culture; proliferation;
 KW epithelial cell; differentiation; T-lymphocyte; African green monkey;

KM primer; PCR; polymerase chain reaction; amplification; probe; ss.

XX Synthetic.

XX US5552303-A.

PN 03-SEP-1996.

XX 08-MAR-1993; 93US-0031399.

XX 08-MAR-1993; 93US-0031399.

PA (IMMV) IMMUNEX CORP.

PI Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;

DR WPI; 1996-412063/41.

PT New isolated simian and human epithelium-derived T-cell factors -
 PT which stimulate the proliferation and/or differentiation of
 PT T-lymphocytes and T-cell lines

XX Example 3; Column 17; 22pp; English.

XX Primers AAT42244-6 were used to amplify a 92 bp fragment of the African
 CC green monkey epithelium-derived T-cell factor (ETF; AAT42243). The
 CC sequence of this primer is based on amino acids 26-31 of the mature ETF
 CC protein sequence obtained by peptide sequencing the purified protein.
 CC The template for the amplification was cDNA derived from monkey kidney
 CC CV-1/EBNA cells stimulated to proliferate by phorbol 12-myristate
 CC 13-acetate. The 92 bp fragment was labelled and used as a probe to
 CC isolate a clone c85.SEF which contained the simian gene. ETF is a
 CC protein of 15-17 kD which is expressed by epithelial cells and
 CC stimulates proliferation and/or differentiation of precursor and/or
 CC mature T cells. The protein is therefore useful for promoting long term
 CC in vivo culture of T-lymphocytes and T-cell lines.

XX Sequence 17 BP: 3 A; 3 C; 2 G; 4 T; 5 other;

Query Match 81.2%; Score 13.8; DB 17; Length 17;
 Best Local Similarity 100.0%; Pred. No. 83;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGCAATCNGTCTTA 17
 |||||||
 DB 1 acrtcngaytcngtrta 17

RESULT 5

AAV02876
 ID AAV02876 standard; DNA: 17 BP.

AC AAV02876;

DT 08-MAY-1998 (first entry)

DE Simian epithelium derived T-cell factor PCR primer 2.

XX Epithelium derived T-cell factor; ETF; simian; gastrointestinal disease;
 KW B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;

KM treatment; prevention; PCR primer; ss.

XX Synthetic.

XX Simian.

XX US5707616-A.

PN 13-JAN-1998.

XX 04-OCT-1996; 96US-0726817.

XX 22-FEB-1995; 95US-0393305.

XX 08-MAR-1993; 93US-0031399.

XX 22-APR-1994; 94US-0233606.

PA (IMMV) IMMUNEX CORP.

PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;

DR WPI; 1998-100295/09.

PT Treatment or prevention of gastrointestinal diseases - by
 PT administering epithelium-derived T-cell factor polypeptide

XX Example 3; Column 41-42; 34pp; English.

XX PCR primers AAV02875-V02877 are used in the amplification of a simian
 CC epithelium-derived T-cell factor (ETF) which is used in a method for
 CC treating or preventing gastrointestinal disease. These polypeptides have
 CC particular application in the treatment of gastrointestinal disorders
 CC associated with disruption of the gastrointestinal epithelium or villi
 CC such as chemotherapy- and radiation-therapy induced enteritis (gut
 CC toxicity), mucositis, peptic ulcer disease, gastroenteritis and colitis,
 CC villus atrophic disorders, malignancy and inflammatory bowel disease.
 CC ETF polypeptides may also be useful in the treatment of human
 CC immunodeficiency virus (HIV) and HIV-associated disease due to their
 CC ability to stimulate CD4+ and CD8+ cells. Biologically active ETF may be
 CC used to treat a variety of other diseases or conditions where T-cell or
 CC B-cell stimulation is desired.

XX Sequence 17 BP: 3 A; 3 C; 2 G; 4 T; 5 other;

Query Match 81.2%; Score 13.8; DB 19; Length 17;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGCAATCNGTCTTA 17
 |||||||
 DB 1 acrtcngaytcngtrta 17

RESULT 6

XX WPI: 1995-373556/48.

DR Isolated DNA encoding polypeptide with mammalian IL-15 activity - which
XX stimulates proliferation and differentiation of T cells, used for
PT treating carcinoma(s), melanomas, etc. and viral infections
PS

XX Example: Page 21, 48pp; English.

CC A simian species of IL-15 (sIL-15) was purified and analysed by SDS-
CC PAGE. Bioassay of unstained gel slices indicated IL-15 activity was
CC Assoc. with proteins having mol. wts in the range of 15-17 kDa. The
CC N-terminus of the first 33 AAs of AAR83309. The results indicated the
CC identity of the first 33 AAs of AAR83309. Subsequent sequencing of a
CC cDNA clone obt. from a simian library provided a sequence encoding
CC the polypeptide AAR83436. AAR83436 comprises a relatively short 48 AA
CC leader sequence and a mature polypeptide AAR83309. The sequence of the
CC N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers
CC for the amplification of IL-15-specific DNA sequences. The first
CC 6 AAs of the N-terminus were used to design one primer, a
CC degenerate mixture coding for all possible codon usages - AAT00528.
CC The AA sequences of the simian mature N-terminus 26-31 were used
CC to design a second primer, a degenerate mixture coding for a
CC complement of all possible codon usages of AAs 26-31, omitting
CC postn. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA
CC cells were used as templates. A 92 bp DNA fragment was used as a
CC hybridism. probe to screen a portion of a plasmid library contg.
CC cDNA inserts prep. from CV-1/EBNA polyadenylated RNA. This
CC resulted in the isolation of clone C85, sIL-15 that has an ORF
CC given in AAT00524. AAR83309 is the active polypeptide & AAR83436 is
CC the precursor polypeptide.

XX Sequence 17 BP; 3 A; 3 C; 2 G; 4 T; 5 other;

Query Match 81.2%; Score 13.8; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTCNGAYTCNGTCTTA 17
| | | | | | | | | | | | | | | | | | |
Db 1 acrtcngaytcngtctta 17

RESULT 2

AA084586 ID AA084586 standard; cDNA; 17 BP.

XX AA084586;

DT 04-SEP-1995 (first entry)

XX Simian IL-15 primer.

XX Interleukin-15; IL-15; sIL-15; T-cell growth factor;

KW African green monkey; CV-1; antitumor; virucide; primer; PCR;

XX polymerase chain reaction; ss.

XX Synthetic.

XX ZA9402636-A.

XX 28-DEC-1994.

XX 18-APR-1994; 94ZA-0002636.

XX 18-APR-1994; 94ZA-0002636.

PI (IMMV) IMMUNEX CORP.

PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;

PI Rauch C;

DR WPI: 1995-082473/11.

XX New purified interleukin-15 - which induces T cell proliferation
PT and differentiation, used for the treatment of tumours and viral
PT infection
PS

XX Example 3; Page 21, 47pp; English.

CC cDNA generated from PMA-stimulated CV-1/EBNA cells was amplified
CC by PCR using primers (AA084585-87) based on the N-terminal sequence
CC of simian interleukin-15 (sIL-15). A clone encoding sIL-15 was
CC obtained (AA084583).

XX Sequence 17 BP; 3 A; 3 C; 2 G; 4 T; 5 other;

Query Match 81.2%; Score 13.8; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTCNGAYTCNGTCTTA 17
| | | | | | | | | | | | | | | | | | |
Db 1 acrtcngaytcngtctta 17

RESULT 3

AA084586 ID AA084586 standard; cDNA; 17 BP.

XX AA084586;

DT 11-MAR-1997 (first entry)

XX Epithelium derived T cell factor PCR primer.

XX Simian epithelium derived T cell factor; sETF; African green monkey;

KW Cercopithecus aethiops; CV1/EBNA cell; T-cell; B-cell; lymphocyte;

KW proliferation; differentiation; gastrointestinal; HIV infection;

XX human immunodeficiency virus; polymerase chain reaction; ss.

XX Synthetic.

XX US5574138-A.

XX 12-NOV-1996.

XX 08-MAR-1993; 93US-0031399.

XX 22-FEB-1995; 95US-0393305.

XX 08-MAR-1993; 93US-0031399.

XX 22-APR-1994; 94US-0233606.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;

XX Rauch C;

XX WPI: 1996-517923/51.

XX New epithelium derived T cell factor - induces proliferation of T

PT and B cells, stimulates destruction of tumour and virus-infected

PT cells and protects against toxicity, partic. for treating intestinal

PT disease and HIV infection

XX Example 3; Column 25; 35pp; English.

XX The simian ETF (epithelium derived T cell factor) was isolated from

CC African green monkey CV1/EBNA cell conditioned medium. The N-

CC terminal sequence of the purified sETF was determined and then PCR

CC primers were designed based on the sequence information. The

CC present sequence is that of a degenerate primer based on amino acids

CC 26-31. 1 e³ Tyr-Thr-Glu-Ser-Asp-Val. A 92 bp fragment was

CC amplified from CV1/EBNA DNA and was used as a probe to screen a

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 02:20:51 ; Search time 291.55 Seconds
(without alignments)
100.112 million cell updates/sec

Title: US-09-724-841-10

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Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.8	81.2	17	16	AAU00529
2	13.8	81.2	17	16	AAQ84586
3	13.8	81.2	17	17	AAU94548
4	13.8	81.2	17	17	AAU42245
5	13.8	81.2	17	19	AAU02876
6	13.8	81.2	17	20	AAU29484
7	13.8	81.2	17	21	AAU38247
8	13.8	81.2	17	22	AAU57022
9	13.8	81.2	23	23	AAU56068

C 10	13.8	81.2	1140	21	AAC98828	Human pancreatic c
C 11	13.8	81.2	1199	22	AAH01023	Streptococcus pneu
C 12	13.8	81.2	1260	20	AAZ35943	Streptococcus pneu
C 13	13.8	81.2	1260	20	AAZ35944	Streptococcus pneu
C 14	13.8	81.2	1260	20	AAZ35945	Streptococcus pneu
C 15	13.8	81.2	1260	20	AAZ35946	Streptococcus pneu
C 16	13.8	81.2	1260	20	AAZ35947	Streptococcus pneu
C 17	13.8	81.2	1552	21	AAU53926	Adenyl cyclase C
C 18	13.8	81.2	1835	23	AAU56071	DNA encoding novel
C 19	13.8	81.2	2092	17	AAU14529	Human adenyl cycl
C 20	13.8	81.2	3343	22	AAU60763	Human polynucleot
C 21	13.8	81.2	4008	17	AAU14528	Rat adenyl cyclase
C 22	13.8	81.2	4008	17	AAU3919	Adenyl cyclase t
C 23	13.8	81.2	4011	22	AAU06820	Human adenylate cy
C 24	13.8	81.2	5717	19	AAU52235	Streptococcus pneu
C 25	12.8	75.3	255	22	AAU82129	Rat differential t
C 26	12.8	75.3	318	22	AAU88626	Escherichia coli p
C 27	12.8	75.3	413	22	AAU07610	Human ovarian and
C 28	12.8	75.3	413	22	AAU02192	Human reproductive
C 29	12.8	75.3	1158	21	AAU07574	Fusarium venenatum
C 30	12.8	75.3	1233	22	AAU65158	Human immune/haema
C 31	12.8	75.3	1233	22	AAU88809	Escherichia coli p
C 32	12.8	75.3	1378	22	AAU88908	Escherichia coli p
C 33	12.8	75.3	1588	17	AAU31005	Rat cardiac alpha
C 34	12.8	75.3	1906	19	AAU59637	Human secreted pro
C 35	12.8	75.3	2404	23	AAU04507	Drosophila melanog
C 36	12.8	75.3	2436	19	AAU59776	Human secreted pro
C 37	12.8	75.3	2474	21	AAU94266	Mung bean ACC synt
C 38	12.8	75.3	2483	23	AAU27452	Drosophila melanog
C 39	12.8	75.3	3503	23	AAU25371	Drosophila melanog
C 40	12.8	75.3	3747	19	AAU05714	Maize retinoblasto
C 41	12.8	75.3	3747	19	AAU17081	Maize retinoblasto
C 42	12.8	75.3	4804	23	AAU46086	CDNA encoding a re
C 43	12.8	75.3	5166	23	AAU04506	Drosophila melanog
C 44	12.8	75.3	8483	23	AAU25370	Drosophila melanog
C 45	12.8	75.3	18796	23	AAU59517	Propionibacterium

ALIGNMENTS

RESULT 1	
AAU00529	AAU00529 standard; cDNA; 17 BP.
ID	AAU00529
XX	AAU00529;
AC	02-FEB-1996 (first entry)
XX	
DT	02-FEB-1996 (first entry)
XX	
DE	Degenerate PCR primer based on simlan IL-15 mature N-terminus 26-31.
XX	
KW	Interleukin-15; epithelium-derived T-cell factor; T lymphocyte;
KM	PCR primer: ss.
XX	
OS	Synthetic.
XX	
FH	Key
FT	misc-feature
FT	1..17
XX	Location/Qualifiers
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XX	/note= "std IUPAC codes used"
PN	WO9527722-A.
PD	19-OCT-1995.
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PF	06-APR-1994; 94WO-US03793.
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PR	06-APR-1994; 94WO-US03793.
XX	
PA	(IMMUNEX CORP.
XX	
XX	Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI	Rauch C;

REFERENCE 2 (sites)
AUTHORS Asahi, Y. and Ubukata, K.
TITLE Association of a thr-371 substitution in a conserved amino acid motif of penicillin-binding protein 1A with penicillin resistance of Streptococcus pneumoniae
JOURNAL Antimicrob. Agents Chemother. 42 (9), 2267-2273 (1998)
MEDLINE 98409715
FEATURES
source Location/Qualifiers
1. 1195
/organism="Streptococcus pneumoniae"
/isolate="#23/HSB21"
/db_xref="taxon:1313"
1. 1195
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/protein_id="BAA32074.1"
/db_xref="GI:3393660"
/translation="VAYPDELQVASTIVDVSNKKVIAQLGARHOSNVSPGICQAVE
TNRDWSGTMKPTITDYAPALEYGVDSATIVHDEPYNPGEDTPYNNDRGFGNITL
QYALQOSRNPVAVETLNKGLNRAKTFNGIDYPSLHYSNAISSNTTESDKKYGAS
SEKMAAAYAAAFANGGTYKKPMYIHKVVSDDSEKESVNGTRAKETTAIYMTDMKT
VLVYIGRGAYLPMIPQAGKTGTSNTYDDEIEKTIKNTGYAPDEMFGYTRKYMAY
WTGYSNRLPLVGDGLTYAAKVRNSMTYLSBGSNPEDMNPEGLYRNGEVEFKNGAR
STWSPAPQPPSTESSSSSDSSSTPSSTPSTNNSTTPNNNTQOQSNTPPOON
ONPQPA"
BASE COUNT 379 a 289 c 240 g 286 t 1 others
ORIGIN

Query Match 81.2%; Score 13.8; DB 1; Length 1195;
Best Local Similarity 70.6%; Pred. No. 4.9e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTCGAYTCNGTRTA 17
11:11 11:11 11:11
DB 678 ACGTCGATTCGCTATA 662

RESULT 15
AB006879/c
LOCUS
DEFINITION Streptococcus pneumoniae pbp1a gene for penicillin binding protein 1A, partial cds, isolate:#24/TJ25, #26/TJ29.
ACCESSION AB006879.1 GI:3395661
VERSION
KEYWORDS pbp1a; penicillin binding protein 1A.
SOURCE Streptococcus pneumoniae (isolate:#24/TJ25, #26/TJ29) DNA.
ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus.
1 (bases 1 to 1195)
Asahi, Y.
REFERENCE
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (27-AUG-1997) Yasuko Asahi, Teikyo University School of Medicine, Department of Clinical Pathology, 2-11-1 Kaga, Itabashi-ku, Tokyo 173-8605, Japan
(E-mail:asahi@med.teikyo-u.ac.jp, Tel:81-3-3964-1211, Fax:81-3-3963-6023)
2 (sites)
Asahi, Y. and Ubukata, K.
REFERENCE
AUTHORS
TITLE Association of a thr-371 substitution in a conserved amino acid motif of penicillin-binding protein 1A with penicillin resistance of Streptococcus pneumoniae
JOURNAL Antimicrob. Agents Chemother. 42 (9), 2267-2273 (1998)
MEDLINE 98409715
FEATURES
source Location/Qualifiers
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/isolate="#24/TJ25, #26/TJ29"

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/codon_start=1
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TNRDWSGTMKPTITDYAPALEYGVDSATIVHDEPYNPGEDTPYNNDRGFGNITL
QYALQOSRNPVAVETLNKGLNRAKTFNGIDYPSLHYSNAISSNTTESDKKYGAS
SEKMAAAYAAAFANGGTYKKPMYIHKVVSDDSEKESVNGTRAKETTAIYMTDMKT
VLVYIGRGAYLPMIPQAGKTGTSNTYDDEIEKTIKNTGYAPDEMFGYTRKYMAY
WTGYSNRLPLVGDGLTYAAKVRNSMTYLSBGSNPEDMNPEGLYRNGEVEFKNGAR
STWSPAPQPPSTESSSSSDSSSTPSSTPSTNNSTTPNNNTQOQSNTPPOON
ONPQPA"
BASE COUNT 378 a 292 c 241 g 284 t
ORIGIN

Query Match 81.2%; Score 13.8; DB 1; Length 1195;
Best Local Similarity 70.6%; Pred. No. 4.9e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTCGAYTCNGTRTA 17
11:11 11:11 11:11
DB 678 ACGTCGATTCGCTATA 662

Search completed: June 19, 2002, 02:54:34
Job time: 7092 sec

ORIGIN

Query Match 81.2% Score 13.8: DB 1: Length 930;
 Best Local Similarity 70.6% Pred. No. 4.9e+02;
 Matches 12: Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17
 ||:| | | | | | | | | |
 Db 708 ACGTCCGATTCGCTATA 692

RESULT 12 AF046234 930 bp DNA linear BCT 30-JUN-1998
 AF046234/c LOCUS Streptococcus pneumoniae strain 56739 penicillin-binding protein 1A
 DEFINITION (ponA) gene, partial cds.
 ACCESSION AF046234.1 GI:2911413
 VERSION AF046234.1
 KEYWORDS Streptococcus pneumoniae.
 SOURCE Streptococcus pneumoniae.
 ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 Streptococcus.

REFERENCE 1 (bases 1 to 930)
 AUTHORS Smith,A.M. and Klugman,K.P.
 TITLE Alterations in PBP 1A essential for high-level penicillin resistance in Streptococcus pneumoniae
 JOURNAL Antimicrob. Agents Chemother. 42 (6), 1329-1333 (1998)
 MEDLINE 98287565
 REFERENCE 2 (bases 1 to 930)
 AUTHORS Smith,A.M.
 TITLE Direct Submission
 JOURNAL Submitted (06-FEB-1998) Microbiology, SAIR Hospital, Johannesburg, Gauteng 2000, South Africa

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gene
 CDS
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BASE COUNT 288 a 216 c 196 g 230 t
 ORIGIN

Query Match 81.2% Score 13.8: DB 1: Length 930;
 Best Local Similarity 70.6% Pred. No. 4.9e+02;
 Matches 12: Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17
 ||:| | | | | | | | | |
 Db 708 ACGTCCGATTCGCTATA 692

RESULT 13 AF046236 930 bp DNA linear BCT 30-JUN-1998
 AF046236/c LOCUS Streptococcus pneumoniae strain N94 penicillin-binding protein 1A
 DEFINITION

(ponA) gene, partial cds.
 ACCESSION AF046236
 VERSION AF046236.1 GI:2911417
 KEYWORDS Streptococcus pneumoniae.
 SOURCE Streptococcus pneumoniae.
 ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 Streptococcus.

REFERENCE 1 (bases 1 to 930)
 AUTHORS Smith,A.M. and Klugman,K.P.
 TITLE Alterations in PBP 1A essential for high-level penicillin resistance in Streptococcus pneumoniae
 JOURNAL Antimicrob. Agents Chemother. 42 (6), 1329-1333 (1998)
 MEDLINE 98287565
 REFERENCE 2 (bases 1 to 930)
 AUTHORS Smith,A.M.
 TITLE Direct Submission
 JOURNAL Submitted (06-FEB-1998) Microbiology, SAIR Hospital, Johannesburg, Gauteng 2000, South Africa

FEATURES
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 1. 930
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 /db_xref="GI:2911417"
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gene
 CDS
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BASE COUNT 287 a 213 c 201 g 229 t
 ORIGIN

Query Match 81.2% Score 13.8: DB 1: Length 930;
 Best Local Similarity 70.6% Pred. No. 4.9e+02;
 Matches 12: Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17
 ||:| | | | | | | | | |
 Db 708 ACGTCCGATTCGCTATA 692

RESULT 14 AB006878 1195 bp DNA linear BCT 13-FEB-1999
 AB006878/c LOCUS Streptococcus pneumoniae pbp1a gene for penicillin binding protein 1A, partial cds. Isolate:#23/HSB21.
 DEFINITION
 ACCESSION AB006878
 VERSION AB006878.1 GI:3395659
 KEYWORDS pbp1a; penicillin binding protein 1A.
 SOURCE Streptococcus pneumoniae (isolate:#23/HSB21) DNA.
 ORGANISM Streptococcus pneumoniae
 Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 Streptococcus.

REFERENCE 1 (bases 1 to 1195)
 AUTHORS Asahi,Y.
 TITLE Direct Submission
 JOURNAL Submitted (27-APR-1997) Yasuko Asahi, Teikyo University School of Medicine, Department of Clinical Pathology, 2-11-1 Kaga, Itabashi-ku, Tokyo 173-8605, Japan
 (E-mail:asahi@med.teikyo-u.ac.jp, Tel:81-3-3964-1211, Fax:81-3-3963-6023)

```

AUTHORS      Smith,A.M. and Klugman,K.P.
TITLE        Alterations in PBP 1A essential for high-level penicillin
JOURNAL      resistance in Streptococcus pneumoniae
MEDLINE      98287565
REFERENCE    2 (bases 1 to 930)
AUTHORS      Smith,A.M.
TITLE        Direct Submission
JOURNAL      Submitted (06-FEB-1998) Microbiology, SAHMR Hospital, Johannesburg,
FEATURES     Location/Qualifiers
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            /db_xref="GI:2911408"
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            TESKKKGCASSEKMAAYAAAFANGCTYKKPKYHKKYVSDSESEFSSVGRRAKETTT
            AYKMTDMKATVLYIGTRGAILPMLPQAGKGSINYDELETENIKMTGYAPDEMFV
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BASE COUNT  283 a      217 c      201 g      229 t

ORIGIN
Query Match      81.2%; Score 13.8; DB 1; Length 930;
Best Local Similarity 70.6%; Pred. No. 4.9e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1  ACRTGCGAYTCNGRTA 17
        ||:||||:|:|:|:|
Db      708  ACGTCGCGATTCGGATA 692

RESULT  10
AF046232      930 bp      DNA      linear      BCT 30-JUN-1998
LOCUS      AF046232/3
DEFINITION      Streptococcus pneumoniae strain 43 penicillin-binding protein 1A
            (ponA) gene, partial cds.
ACCESSION      AF046232
VERSION      AF046232.1  GI:2911409
KEYWORDS
SOURCE
ORGANISM      Streptococcus pneumoniae.
            Streptococcus pneumoniae
            Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
            Streptococcus.
REFERENCE
AUTHORS      Smith,A.M. and Klugman,K.P.
TITLE        Alterations in PBP 1A essential for high-level penicillin
JOURNAL      resistance in Streptococcus pneumoniae
MEDLINE      98287565
REFERENCE    2 (bases 1 to 930)
AUTHORS      Smith,A.M.
TITLE        Direct Submission
JOURNAL      Submitted (06-FEB-1998) Microbiology, SAHMR Hospital, Johannesburg,
FEATURES     Location/Qualifiers
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gene
CDS

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BASE COUNT	284 a 214 c 202 g 230 t
ORIGIN	
Query Match	81.2% Score 13.8; DB 1; Length 930;
Best Local Similarity	70.6%; Pred. No. 4.9e+02;
Matches	12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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RESULT 11	
AF046233/c	930 bp DNA linear BCT 30-JUN-1998
LOCUS	Streptococcus pneumoniae strain 64429 penicillin-binding protein 1A
DEFINITION	(pona) gene, partial cds.
ACCESSION	AF046233
VERSION	AF046233.1 GI:2911411
KEYWORDS	
SOURCE	Streptococcus pneumoniae.
ORGANISM	Streptococcus pneumoniae. Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus.
REFERENCE	1 (bases 1 to 930)
AUTHORS	Smith,A.M. and Klugman,K.P.
TITLE	Alterations in PBP 1A essential for high-level penicillin resistance in Streptococcus pneumoniae
JOURNAL	Antimicrob. Agents Chemother. 42 (6), 1329-1333 (1998)
MEDLINE	98287565
REFERENCE	2 (bases 1 to 930)
AUTHORS	Smith,A.M.
TITLE	Direct Submission
JOURNAL	Submitted (06-FEB-1998) Microbiology, SAIMR Hospital, Johannesburg, Gauteng 2000, South Africa
FEATURES	Location/Qualifiers
source	1..930 /organism="Streptococcus pneumoniae" /strain="64429" /db_xref="taxon:1313" <1..>930 /gene="pona" <1..>930 /note="PBP 1A" /codon_start=1 /transl_table=11 /product="penicillin-binding protein 1A" /protein_id="AAC24698.1" /db_xref="GI:2911412" /translation="LMDIYNTDEVAVYPDELOVASTIVDSNGKVIAQLGARHSSNSVSFGINAVENFRDMGSTMKPTIDYPALEGVYDSTATIVHDEPNVPYPCGDTPVNMNDRGEFGITTLQALQOSRNVPAVE TLKKVGINRAKTFLNGIGIDIPSIHSNATLSNTTTSBKTKGASSEKMAAAVAAPANGGTYYKPMYIKHVYSDESSESNGVRARKEETTYAHMTDMAKTVLYVIGIRGAYILPALPGAQKGTSNYTDEIEIKINIGYVADPEMFVGYTKKIYAAVWTGSNNRLTFLVGGTLVAARKYR"
CDS	
gene	
BASE COUNT	288 a 215 c 198 g 229 t

ORIGIN

Query Match 81.2%; Score 13.8; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGATCNGTGT 17
Db 1 ACRTGATCNGTGT 17

RESULT 7

AF233548 350 bp DNA linear INV 16-FEB-2001
LOCUS Ballochia hildegarda wingless (wg) gene, partial cds.
DEFINITION AF233548
ACCESSION AF233548 GI:12863151
VERSION
KEYWORDS
SOURCE Ballochia hildegarda.
ORGANISM Ballochia hildegarda.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
Ditrysia; Papilionoidea; Lycaenidae; Fortitinae; Liptenini;
Ballochia.

REFERENCE 1 (bases 1 to 350)
AUTHORS Campbell,D.L., Brower,A.V. and Pierce,N.E.
TITLE Molecular evolution of the wingless gene and its implications for the phylogenetic placement of the butterfly family Riodinidae (Lepidoptera: Papilionoidea)

JOURNAL Mol. Biol. Evol. 17 (5), 684-696 (2000)

REFERENCE 2 (bases 1 to 350)
AUTHORS Campbell,D.L., Brower,A.V.Z. and Pierce,N.E.
TITLE Direct Submission

JOURNAL Submitted (11-FEB-2000) Organismic and Evolutionary Biology,
Harvard University, 26 Oxford St., Cambridge, MA 02138, USA
COMMENT On Feb 16, 2001 this sequence version replaced g1:7804846.

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BASE COUNT 101 a 78 c 88 g 83 t
ORIGIN

Query Match 81.2%; Score 13.8; DB 3; Length 350;
Best Local Similarity 70.6%; Pred. No. 5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGATCNGTGT 17
Db 243 ACATCAGACTCGGTATA 259

RESULT 8

AC038651 standard; DNA; HTG; 850 BP.
XX AC038651;
XX AC038651;
SV AC038651.1

XX

10-APR-2000 (Rel. 63, Created)

DT

10-APR-2000 (Rel. 63, Last updated, Version 1)

XX

Giardia intestinalis clone EJ2784 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.

DE

HTG; HTGS_PHASE0.

XX

Giardia intestinalis

OS

Eukaryota; Diplomonadida; Hexamitidae; Giardinales; Giardia.

OC

[1]

XX

Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C.,

RP

Hinkle G., Holder M.E., Sogin M.L.;

RA

Submitted (10-APR-2000) to the EMBL/GenBank/DBJ databases.

RL

Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA

RL

unpublished.

XX

[2]

XX

Eakin N.Q., Morrison H.G., McArthur A.G., Nixon J., Kim U., Crocker M.C.,

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Hinkle G., Holder M.E., Sogin M.L.;

RA

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RL

unpublished.

XX

[2]

XX

Eakin N.Q., Morrison H.G., McArthur A.G., Nixon J., Kim U., Crocker M.C.,

RP

Hinkle G., Holder M.E., Sogin M.L.;

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Submitted (10-APR-2000) to the EMBL/GenBank/DBJ databases.

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RL

unpublished.

XX

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XX

Eakin N.Q., Morrison H.G., McArthur A.G., Nixon J., Kim U., Crocker M.C.,

RP

Hinkle G., Holder M.E., Sogin M.L.;

RA

Submitted (10-APR-2000) to the EMBL/GenBank/DBJ databases.

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Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA

RL

unpublished.

XX

[2]

XX

Eakin N.Q., Morrison H.G., McArthur A.G., Nixon J., Kim U., Crocker M.C.,

RP

Hinkle G., Holder M.E., Sogin M.L.;

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Submitted (10-APR-2000) to the EMBL/GenBank/DBJ databases.

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Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA

RL

unpublished.

XX

[2]

XX

Eakin N.Q., Morrison H.G., McArthur A.G., Nixon J., Kim U., Crocker M.C.,

RP

Hinkle G., Holder M.E., Sogin M.L.;

RA

Submitted (10-APR-2000) to the EMBL/GenBank/DBJ databases.

RL

Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA

RL

unpublished.

XX

[2]

XX

Eakin N.Q., Morrison H.G., McArthur A.G., Nixon J., Kim U., Crocker M.C.,

RP

Hinkle G., Holder M.E., Sogin M.L.;

RA

Submitted (10-APR-2000) to the EMBL/GenBank/DBJ databases.

RL

Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA

RL

unpublished.

XX

[2]

XX

Eakin N.Q., Morrison H.G., McArthur A.G., Nixon J., Kim U., Crocker M.C.,

RP

Hinkle G., Holder M.E., Sogin M.L.;

RA

Submitted (10-APR-2000) to the EMBL/GenBank/DBJ databases.

RL

Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA

RL

unpublished.

XX

[2]

XX

Eakin N.Q., Morrison H.G., McArthur A.G., Nixon J., Kim U., Crocker M.C.,

RP

Hinkle G., Holder M.E., Sogin M.L.;

RA

Submitted (10-APR-2000) to the EMBL/GenBank/DBJ databases.

RL

Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17
 DB 1 ACRTGNGAYTCNGTRTA 17

RESULT 2
 LOCUS AR070286 17 bp DNA PAT 18-FEB-2000
 DEFINITION Sequence 10 from patent US 5892001.
 ACCESSION AR070286
 VERSION AR070286.1 GI:7221174
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
 TITLE Epithelium-derived T-cell factor antibodies
 JOURNAL Patent: US 5892001-A 10 06-APR-1999;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"

BASE COUNT 3 a 3 c 2 g 4 t 5 others

ORIGIN

Query Match 81.2%; Score 13.8; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17
 DB 1 ACRTGNGAYTCNGTRTA 17

RESULT 3
 LOCUS AR085745 17 bp DNA PAT 07-SEP-2000
 DEFINITION Sequence 10 from patent US 5985262.
 ACCESSION AR085745
 VERSION AR085745.1 GI:10012511
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
 TITLE Method of treatment with epithelium derived T-cell factor
 JOURNAL Patent: US 5985262-A 10 16-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"

BASE COUNT 3 a 3 c 2 g 4 t 5 others

ORIGIN

Query Match 81.2%; Score 13.8; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17
 DB 1 ACRTGNGAYTCNGTRTA 17

RESULT 4
 LOCUS 125787 17 bp DNA PAT 07-OCT-1996
 DEFINITION Sequence 10 from patent US 5552303.
 ACCESSION 125787
 VERSION 125787.1 GI:1605657

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Grabstein,K.H., Anderson,D., Eisenman,J., Fung,V. and Rauch,C.
 TITLE DNA encoding epithelium-derived T-cell factor
 JOURNAL Patent: US 5552303-A 10 03-SEP-1996;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"

BASE COUNT 3 a 3 c 2 g 4 t 5 others

ORIGIN

Query Match 81.2%; Score 13.8; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17
 DB 1 ACRTGNGAYTCNGTRTA 17

RESULT 5
 LOCUS 128854 17 bp DNA PAT 06-FEB-1997
 DEFINITION Sequence 10 from patent US 5574138.
 ACCESSION 128854
 VERSION 128854.1 GI:1819636
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
 TITLE Epithelium-derived T-cell factor
 JOURNAL Patent: US 5574138-A 10 12-NOV-1996;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"

BASE COUNT 3 a 3 c 2 g 4 t 5 others

ORIGIN

Query Match 81.2%; Score 13.8; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17
 DB 1 ACRTGNGAYTCNGTRTA 17

RESULT 6
 LOCUS 179224 17 bp DNA PAT 10-JUN-1998
 DEFINITION Sequence 10 from patent US 5707616.
 ACCESSION 179224
 VERSION 179224.1 GI:3207514
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
 TITLE Method for treating or preventing gastrointestinal disease with
 epithelium-derived T-cell factor
 JOURNAL Patent: US 5707616-A 10 13-JUN-1998;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"

BASE COUNT 3 a 3 c 2 g 4 t 5 others

ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Word for Windows 95, 7.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,317B
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2831
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-08-392-317B-9

Query Match 80.0%; Score 14.4; DB 1; Length 69;
Best Local Similarity 72.2%; Pred. No. 8.3;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Caps 0;
OY 1 AAYTGGTNAAYGTNATH 18
Db 49 AACTGGTCAATCTAATA 66

Search completed: June 19, 2002, 02:22:11
Job time: 5419 sec

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-09-134-134A-7

Query Match 80.0%; Score 14.4; DB 4; Length 39;
Best Local Similarity 72.2%; Pred. No. 7.6;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGTNAAYGTNATH 18
||:||||| ||:| ||:
DB 22 AACTGGGTCAATGTATA 39

RESULT 13
US-09-134-456-7
Sequence 7, Application US/09134456
Patent No. 6168783
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Paxton, Raymond
TITLE OF INVENTION: Antagonists of IL-15
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Word for Windows 95, 7.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,456
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/392,317
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2831
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-09-134-456-7

Query Match 80.0%; Score 14.4; DB 4; Length 39;
Best Local Similarity 72.2%; Pred. No. 7.6;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGTNAAYGTNATH 18
||:||||| ||:| ||:
DB 22 AACTGGGTCAATGTATA 39

RESULT 14
US-09-196-427-7
Sequence 7, Application US/09196427
Patent No. 6177079
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Paxton, Raymond
TITLE OF INVENTION: Antagonists of IL-15
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Word for Windows 95, 7.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,427
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/392,317
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2831
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-09-196-427-7

Query Match 80.0%; Score 14.4; DB 4; Length 39;
Best Local Similarity 72.2%; Pred. No. 7.6;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGTNAAYGTNATH 18
||:||||| ||:| ||:
DB 22 AACTGGGTCAATGTATA 39

RESULT 15
US-08-392-317B-9
Sequence 9, Application US/08392317B
Patent No. 5795966
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Paxton, Raymond
TITLE OF INVENTION: Antagonists of IL-15
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA

DB 8 AACTGGGTGAATGTATA 25

RESULT 10

US-08-392-317B-7
Sequence 7, Application US/08392317B
Patent No. 5795966

GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth
APPLICANT: Paxton, Raymond

TITLE OF INVENTION: Antagonists of IL-15

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Word for Windows 95, 7.0

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/392,317B

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2831

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0430

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

US-08-392-317B-7

Query Match

Best Local Similarity 80.0%; Score 14.4; DB 1; Length 39;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DB 22 AACTGGGTGAATGTATA 39

RESULT 11

US-09-134-132-7

Sequence 7, Application US/09134132

Patent No. 6013480

GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth

APPLICANT: Paxton, Raymond

TITLE OF INVENTION: Antagonists of IL-15

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Word for Windows 95, 7.0

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/134,132

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER: US/08/392,317

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2831

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0430

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

US-09-134-132-7

Query Match

Best Local Similarity 80.0%; Score 14.4; DB 3; Length 39;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DB 22 AACTGGGTGAATGTATA 39

RESULT 12

US-09-134-134A-7

Sequence 7, Application US/09134134A

Patent No. 6165466

GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth

APPLICANT: Paxton, Raymond

TITLE OF INVENTION: Antagonists of IL-15

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Word for Windows 95, 7.0

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/134,134A

FILING DATE:

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER: 08/392,317

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2831

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0430

CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,193
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-189-193-9

Query Match 80.0%; Score 14.4; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGGGTNAAYGTNATH 18
DB 1 AAYTGGGTNAAYGTNATH 18

RESULT 8
PCT-US94-03793-9
Sequence 9, Application PC/TUS9403793
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: Interleukin-15
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03793
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Launer, Charlene
REGISTRATION NUMBER: 33,035

REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US94-03793-9

Query Match 80.0%; Score 14.4; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGGGTNAAYGTNATH 18
DB 1 AAYTGGGTNAAYGTNATH 18

RESULT 9
US-08-842-947-1
Sequence 1, Application US/08842947
Patent No. 6001973
GENERAL INFORMATION:
APPLICANT: Strom, Terry B.
APPLICANT: Maslinski, Wlodzislaw
TITLE OF INVENTION: ANTAGONISTS OF INTERLEUKIN-15
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,947
FILING DATE: 25-APR-1997
CLASSIFICATION: 432
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,634
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 01948/039001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-842-947-1

Query Match 80.0%; Score 14.4; DB 3; Length 25;
Best Local Similarity 72.2%; Pred. No. 7.1;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGGTNAAYGTNATH 18

REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-504-042-9

Query Match 80.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 AAYTGGTNAAYGTNATH 18
|||||
Db 1 AAYTGGTNAAYGTNATH 18

RESULT 5
US-08-725-969-9
Sequence 9, Application US/08725969
Patent No. 5892001
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELUM-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,969
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-725-969-9

Query Match 80.0%; Score 14.4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 AAYTGGTNAAYGTNATH 18
|||||
Db 1 AAYTGGTNAAYGTNATH 18

RESULT 6
US-08-794-524-9
Sequence 9, Application US/08794524
Patent No. 5985262
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELUM-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,524
FILING DATE: 03-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-794-524-9

Query Match 80.0%; Score 14.4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 AAYTGGTNAAYGTNATH 18
|||||
Db 1 AAYTGGTNAAYGTNATH 18

RESULT 7
US-09-189-193-9
Sequence 9, Application US/09189193
Patent No. 6184359
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELUM-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15

QY 1 AAYTGGTNAAYGTNATH 18
Db 1 AAYTGGTNAAYGTNATH 18

RESULT 2

US-08-393-305-9
Sequence 9, Application US/08393305
Patent No. 5574138
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Betty
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,305
FILING DATE: 22-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-393-305-9

Query Match 80.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.7;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18
Db 1 AAYTGGTNAAYGTNATH 18

RESULT 3

US-08-726-817-9
Sequence 9, Application US/08726817
Patent No. 5707616
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Betty
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle

STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,817
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-726-817-9

Query Match 80.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18
Db 1 AAYTGGTNAAYGTNATH 18

RESULT 4

US-08-504-042-9
Sequence 9, Application US/08504042
Patent No. 5747024
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: Epithelial-derived T-cell Factor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,042
FILING DATE: 19-JUL-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,399
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Launer, Charlene
REGISTRATION NUMBER: 33,035

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 00:51:52 ; Search time 66.01 Seconds
(without alignments)
66.981 Million cell updates/sec

Title: US-09-724-841-9

Perfect score: 18

Sequence: 1 AAYTGCTNAAVGTNATH 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/lna/5A_COMB.seq:*
4: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
5: /cgn2_6/ptodata/2/lna/5A_COMB.seq:*
6: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	80.0	18	1 US-08-031-399-9	Sequence 9, Appl1
2	14.4	80.0	18	1 US-08-393-305-9	Sequence 9, Appl1
3	14.4	80.0	18	1 US-08-726-817-9	Sequence 9, Appl1
4	14.4	80.0	18	1 US-08-504-042-9	Sequence 9, Appl1
5	14.4	80.0	18	2 US-08-725-969-9	Sequence 9, Appl1
6	14.4	80.0	18	2 US-08-794-524-9	Sequence 9, Appl1
7	14.4	80.0	18	4 US-09-189-193-9	Sequence 9, Appl1
8	14.4	80.0	18	5 PCT-US94-03793-9	Sequence 9, Appl1
9	14.4	80.0	25	3 US-08-842-947-1	Sequence 1, Appl1
10	14.4	80.0	39	1 US-08-392-317B-7	Sequence 7, Appl1
11	14.4	80.0	39	3 US-09-134-132-7	Sequence 7, Appl1
12	14.4	80.0	39	4 US-09-134-134A-7	Sequence 7, Appl1
13	14.4	80.0	39	4 US-09-134-456-7	Sequence 7, Appl1
14	14.4	80.0	39	4 US-09-196-427-7	Sequence 7, Appl1
15	14.4	80.0	69	3 US-08-392-317B-9	Sequence 9, Appl1
16	14.4	80.0	69	3 US-09-134-132-9	Sequence 9, Appl1
17	14.4	80.0	69	4 US-09-134-134A-9	Sequence 9, Appl1
18	14.4	80.0	69	4 US-09-134-456-9	Sequence 9, Appl1
19	14.4	80.0	69	4 US-09-196-427-9	Sequence 9, Appl1
20	14.4	80.0	345	1 US-08-393-305-12	Sequence 12, Appl1
21	14.4	80.0	345	1 US-08-393-305-13	Sequence 13, Appl1
22	14.4	80.0	345	1 US-08-726-817-12	Sequence 12, Appl1
23	14.4	80.0	345	1 US-08-726-817-13	Sequence 13, Appl1
24	14.4	80.0	345	2 US-08-725-969-12	Sequence 12, Appl1
25	14.4	80.0	345	2 US-08-725-969-13	Sequence 13, Appl1
26	14.4	80.0	345	2 US-08-794-524-12	Sequence 12, Appl1
27	14.4	80.0	345	2 US-08-794-524-13	Sequence 13, Appl1

ALIGNMENTS

28	14.4	80.0	345	4 US-09-189-193-12	Sequence 12, Appl1
29	14.4	80.0	345	4 US-09-189-193-13	Sequence 13, Appl1
30	14.4	80.0	489	1 US-08-031-399-1	Sequence 1, Appl1
31	14.4	80.0	489	1 US-08-031-399-4	Sequence 4, Appl1
32	14.4	80.0	489	1 US-08-393-305-1	Sequence 1, Appl1
33	14.4	80.0	489	1 US-08-393-305-4	Sequence 4, Appl1
34	14.4	80.0	489	1 US-08-335-733-1	Sequence 1, Appl1
35	14.4	80.0	489	1 US-08-726-817-1	Sequence 1, Appl1
36	14.4	80.0	489	1 US-08-726-817-4	Sequence 4, Appl1
37	14.4	80.0	489	1 US-08-504-042-1	Sequence 1, Appl1
38	14.4	80.0	489	1 US-08-504-042-4	Sequence 4, Appl1
39	14.4	80.0	489	1 US-08-392-317B-1	Sequence 1, Appl1
40	14.4	80.0	489	1 US-08-392-317B-2	Sequence 2, Appl1
41	14.4	80.0	489	2 US-08-725-969-1	Sequence 1, Appl1
42	14.4	80.0	489	2 US-08-725-969-4	Sequence 4, Appl1
43	14.4	80.0	489	2 US-08-794-524-1	Sequence 1, Appl1
44	14.4	80.0	489	2 US-08-794-524-4	Sequence 4, Appl1
45	14.4	80.0	489	3 US-08-842-947-5	Sequence 5, Appl1

RESULT 1
US-08-031-399-9
Sequence 9, Application US/08031399

Patent No. 5552303

GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth

APPLICANT: Anderson, Dirk

APPLICANT: Eisenman, June

APPLICANT: Rauch, Victor

TITLE OF INVENTION: Epithelium-derived T-cell factor

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/031.399

FILING DATE: 19930308

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Launer, Charlene

REGISTRATION NUMBER: 33,035

REFERENCE/DOCKET NUMBER: 2811

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0430

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-031-399-9

Query Match 80.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Wed Jun 19 09:14:05 2002

us-09-724-841-9.rst

RESULT 14
 LOCUS AO329420 654 bp DNA linear GSS 08-JAN-1999
 DEFINITION nbxb0044p20f CUGI Rice BAC library Oryza sativa genomic clone
 nbxb0044p20f, DNA sequence.
 ACCESSION AO329420
 VERSION AO329420.1 GI:4121270
 KEYWORDS GSS.
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 654)
 Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Rice Genome
 Unpublished (1998)
 JOURNAL Contact: Wing RA
 COMMENT Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Seq primer: TTAATACGACTCACTATAGCG
 Class: BAC ends
 High quality sequence stop: 254.
 Location/Qualifiers
 1..654
 /organism="Oryza sativa"
 /strain="Japonica"
 /cultivar="Nipponbare"
 /db_xref="taxon:4530"
 /clone="nbxb0044p20f"
 /clone_lib="CUGI Rice BAC Library"
 /tissue_type="Leaf"
 /lab_host="E. coli DH10B"
 /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
 HindIII; Rice is one of two most popular grains in the
 world. Half of the world population especially those
 inhabiting highly populated areas of the humid tropics
 and subtropics, rely on rice as their primary source of
 carbohydrate. Monocotyledonous rice is a diploid plant
 (2n=24) with a haploid genome equivalent of 431 Mbp
 (Arumuganathan and Earle, 1991). The relatively small
 genome of rice, three times larger than that of
 Arabidopsis, makes it suitable for genomic studies. In
 order to facilitate positional cloning, physical mapping
 and genome sequencing of rice, we have constructed a BAC
 library from Oryza sativa, Nipponbare variety. The
 library contains 36,864 clones with an average insert size
 of 128.5 Kb providing 10.9 haploid genome equivalents. The
 deep coverage allows the isolation a particular sequence
 with a probability of 99.9%. Two high density filters,
 each containing 18,432 clones (doubly spotted), represent
 the whole library for colony screening."
 BASE COUNT 190 a 83 c 100 g 275 t 6 others
 ORIGIN
 Query Match 80.0%; Score 14.4; DB 12; Length 654;
 Best Local Similarity 72.2%; Pred. No. 1.8e+03;
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAYTGGGTNAAYGTNATH 18
 ||:||||| ||:|||||
 Db 504 AATTGGGTAAATGTAATT 521
 RESULT 15
 LOCUS BF645513 674 bp mRNA linear EST 20-DEC-2000

DEFINITION NF020F02EC1F1026 Elicited cell culture Medicago truncatula cDNA
 clone NF020F02EC 5', mRNA sequence.
 ACCESSION BF645513
 VERSION BF645513.1 GI:11910642
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 REFERENCE 1 (bases 1 to 674)
 Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
 Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation -
 Center for Medicago Genomics Research
 Unpublished (2000)
 JOURNAL Contact: Dixon RA
 COMMENT Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7302
 Fax: 580 221 7380
 Email: radixon@noble.org
 Insert Length: 674 Std Error: 0.00
 Plate: 020 row: F column: 02
 Seq primer: TCACACGAGCAACGCTATGAC.
 Location/Qualifiers
 1..674
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF020F02EC"
 /clone_lib="Elicited cell culture"
 /tissue_type="Cell cultures derived from root tissues"
 /dev_stage="Cell suspensions were subcultured every 14
 days. Cells were induced six days after subculture"
 /note="Vector: Lambda Zap; Cells were induced with yeast
 final wall extracts equivalent to 50ug/ml glucose in the
 24 hours after induction. Samples were taken at 0.5, 1, 12 and
 time point were pooled and used for mRNA isolation."
 BASE COUNT 181 a 165 c 122 g 205 t 1 others
 ORIGIN
 Query Match 80.0%; Score 14.4; DB 10; Length 674;
 Best Local Similarity 72.2%; Pred. No. 1.9e+03;
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AAYTGGGTNAAYGTNATH 18
 ||:||||| ||:|||||
 Db 125 AATTGGGTGAACGTGATT 108
 Search completed: June 19, 2002, 02:15:49
 Job time: 7362 sec

using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

BASE COUNT 171 a 106 c 119 g 188 t
ORIGIN

Query Match 80.0%; Score 14.4; DB 10; Length 584;
Best Local Similarity 72.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGTAAAGTAAATG 18
||:||||| ||:| ||:
Db 513 AACTGGGTCAATGATC 496

RESULT 12
A0947440 600 bp DNA linear GSS 27-JAN-2000
LOCUS Sheared DNA-49K15.TF Sheared DNA Trypanosoma brucei genomic clone
DEFINITION Sheared DNA-49K15, DNA sequence.
ACCESSION A0947440
VERSION A0947440.1 GI:6770705
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 600)
AUTHORS El-Sayed, N., Zhao, H., Gill, S., Sub, E., Malek, J., Fujii, C., Gerard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.
Determination of clone end sequences from Trypanosoma brucei cDNA library

JOURNAL 10.1 Sheared DNA library
COMMENT Unpublished (1999)
Other_GSSs: Sheared DNA-49K15.TR
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: <http://www.tigr.org/tldb/mdb/tldb/>.
Seq primer: M13-Forward
Class: shotgun.

FEATURES
SOURCE Location/Qualifiers

1..600
/organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
/clone="Sheared DNA-49K15"
/clone_lib="Sheared DNA"
/note="Vector: pUC18; Site_1: SmaI; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999)."

BASE COUNT 199 a 127 c 107 g 167 t
ORIGIN

Query Match 80.0%; Score 14.4; DB 12; Length 600;
Best Local Similarity 72.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGTAAAGTAAATG 18
||:||||| ||:| ||:
Db 66 AAYTGGGTCAAGTAAAT 83

RESULT 13
BH098364 609 bp DNA linear GSS 19-JUL-2001
LOCUS RPCI-24-315N8.TJ RPCI-24 Mus musculus genomic clone RPCI-24-315N8, DNA sequence.
DEFINITION RPCI-24-315N8, TJ RPCI-24 Mus musculus genomic clone RPCI-24-315N8, DNA sequence.
ACCESSION BH098364
VERSION BH098364.1 GI:14920086
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 609)
AUTHORS Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akintre, B., Levins, M., Tsagaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebreyegorgis, E., Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-315N8.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdjong@mail.chu.org). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/orderframe.html>). BAC end plate: 315 row: N column: 8
Seq primer: SP6
Class: BAC ends.

FEATURES
SOURCE Location/Qualifiers

1..609
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-315N8"
/clone_lib="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pPARBAC1; Site_1: BamHI; Site_2: BamHI; RPCI-24 Mouse BAC library produced by Pieter de Jong. The library was cloned in the pPARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."

BASE COUNT 229 a 100 c 122 g 158 t
ORIGIN

Query Match 80.0%; Score 14.4; DB 12; Length 609;
Best Local Similarity 72.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGTAAAGTAAATG 18
||:||||| ||:| ||:
Db 558 AATGGGTAAATGTAAT 575

TITLE	R.A.
JOURNAL	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library
COMMENT	Unpublished (2000) Contact: Dixon RA Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7302 Fax: 580 221 7380 Email: radixon@noble.org Insert Length: 560 Std Error: 0.00 Plate: 002 row: F column: 06 Seq primer: TCACACGGAAGAACGTATGC. Location/Qualifiers
FEATURES	Source 1..560 /organism="Medicago truncatula" /db_xref="taxon:3880" /clone="NF002F06ST" /clone_lib="developing stem" /tissue_type="stem" /dev_stage="Pooled developmental" /note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
BASE COUNT	144 a 150 c 91 g 174 t 1 others
ORIGIN	
Query Match	80.0%; Score 14.4; DB 9; Length 560;
Best Local Similarity	72.2%; Pred. No. 1.8e+03;
Matches	13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY	1 AAYTGGGTAAATGYNATH 18 : : :
Db	143 AATTGGTGTAACGTATT 126
RESULT 10	
LOCUS	AQ421826
DEFINITION	RPCI-11-186D1.TV RPCI-11 Homo sapiens genomic clone RPCI-11-186D1, DNA sequence.
ACCESSION	AQ421826
VERSION	AQ421826.1 GI:4479550
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 566)
AUTHORS	Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter J.C.
TITLE	Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL	Unpublished (1997)
COMMENT	Other_GSSs: RPCI-11-186D1.TJ Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@tlgr.org Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (http://resgen.com). BAC end search page: http://www.tlgr.org/tldb/hungen/bac_end_search/bac_end_search.html . Seq primer: T7 Class: BAC ends. Location/Qualifiers 1..566

QUERY MATCH	80.0%	Score 14.4;	DB 12;	Length 566;
Best Local Similarity	72.2%	Pred. No. 1.8e+03;		
Matches 13; Conservative	3;	Mismatches 2;	Indels 0;	Gaps 0;
QY 1	AAATGGGTAAATGTTAAH 18			
Db 468	AATGGGTAAATGTTAAATC 451			
RESULT 11				
BG082266/c		584 bp	mRNA	linear EST 26-JAN-2001
DEFINITION	H3074C12-5 N1A Mouse 15K cDNA Clone Set Mus musculus cDNA clone			
LOCUS	H3074C12.5', mRNA sequence.			
ACCESSION	BG082266			
VERSION	BG082266.1	GI:12564834		
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 584) Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka,T.S., Carter,M.G. and Ko,M.S.H.			
TITLE	Verification and initial annotation of N1A mouse 15K cDNA clone set			
JOURNAL	Unpublished (2001)			
COMMENT	Other_ESTs: H3074C12-3 Contact: George J. Kargul Laboratory of Genetics National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@sgsn.grc.nia.nih.gov This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details. Plate: H3074 row: C column: 12 Seq primer: -21M13 Reverse High quality sequence stop: 584 POLYA-No.			
FEATURES	Location/Qualifiers			
source	1..584			
	/organism="Mus musculus"			
	/strain="C57BL/6J"			
	/db_xref="niaST:H3074C12-5"			
	/db_xref="taxon:10090"			
	/clone="H3074C12"			
	/clone_1lb="N1A Mouse 15K cDNA Clone Set"			
	/sex="Clones arrayed from a variety of cDNA libraries"			
	/dev_stage="Clones arrayed from a variety of cDNA libraries"			
	/lab_host="DH10B"			
	/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos , and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT) -Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo			

NbHPU, and fetal heart NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT 149 a 91 c 108 g 161 t

Query Match 80.0%; Score 14.4; DB 9; Length 509;
Best Local Similarity 72.2%; Pred. No. 1.7e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18
||:||||| ||:| ||:
DB 249 AACTGGTGACGTATATA 266

RESULT 7
BF650545/c 515 bp mRNA linear EST 20-DEC-2000
LOCUS NF090F01EC1F1013 Elicited cell culture Medicago truncatula cDNA
DEFINITION clone NF090F01EC 5', mRNA sequence.
ACCESSION BF650545
VERSION BF650545.1 GI:11915675
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

REFERENCE 1 (bases 1 to 515)
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research
JOURNAL Unpublished (2000)
COMMENT Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org

Insert length: 515 Std Error: 0.00
Plate: 090 row: F column: 01
Seq primer: TCACACAGGAACACGCTATGAC.
FEATURES
Location/Qualifiers
1..515
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF090F01EC"
/clone_lib="Elicited cell culture"
/tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14 days. Cells were induced six days after subculture"
/note="Vector: Lambda zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."

BASE COUNT 135 a 135 c 88 g 157 t

ORIGIN

Query Match 80.0%; Score 14.4; DB 10; Length 515;
Best Local Similarity 72.2%; Pred. No. 1.7e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAYTGGTNAAYGTNATH 18

DB 124 AAYTGGTGACGTAT 107
||:||||| ||:| ||:
RESULT 8
TA241H020/c 547 bp DNA linear GSS 13-DEC-2000
LOCUS T241H020/c
DEFINITION T. brucei sheared genomic DNA clone 241h02, reverse sequence.
ACCESSION AL482700.1 GI:11848562
VERSION AL482700
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei

Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 547)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhlesanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at <http://www.sanger.ac.uk/projects/T-brucei/>.
FEATURES
Location/Qualifiers
1..547
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="241h02"

BASE COUNT 148 a 104 c 105 g 190 t

ORIGIN

Query Match 80.0%; Score 14.4; DB 12; Length 547;
Best Local Similarity 72.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18
||:||||| ||:| ||:
DB 475 AAYTGGTGACGTATATA 458

RESULT 9
AM688129/c 560 bp mRNA linear EST 15-JUN-2000
LOCUS NF002F06ST 5', mRNA sequence.
DEFINITION NF002F06ST 5', mRNA sequence.
ACCESSION AM688129
VERSION AM688129.1 GI:7562788
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

REFERENCE 1 (bases 1 to 560)
He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W., May, G.D. and Dixon

ACCESSION A0154673 GI:3547343
 VERSION A0154673.1
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 487)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3021 row: E column: 15
 Class: BAC ends
 High quality sequence stop: 487.
 Location/Qualifiers
 1..487
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
 E-Coli DH10B"
 BASE COUNT 111 a 136 c 112 g 126 t 2 others
 ORIGIN
 Query Match 80.0%; Score 14.4; DB 12; Length 487;
 Best Local Similarity 72.2%; Pred. No. 1.7e+03;
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 AAYTGGTNAAGTGNATH 18
 ||:||||| ||:|||||
 Db 66 AATTGGTTATGTCATT 49
 RESULT 5
 LOCUS A0132420 490 bp DNA linear GSS 23-SEP-1998
 DEFINITION HS_3021_A1_C08_MR CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone plate=3021 Col=15 Row=E, DNA sequence.
 ACCESSION A0132420
 VERSION A0132420.1 GI:3509586
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 490)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618

Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3021 row: E column: 15
 Class: BAC ends
 High quality sequence stop: 490.
 Location/Qualifiers
 1..490
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
 E-Coli DH10B"
 BASE COUNT 110 a 136 c 113 g 130 t 1 others
 ORIGIN
 Query Match 80.0%; Score 14.4; DB 12; Length 490;
 Best Local Similarity 72.2%; Pred. No. 1.7e+03;
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 AAYTGGTNAAGTGNATH 18
 ||:||||| ||:|||||
 Db 88 AATTGGTNAAGTGNATH 71
 RESULT 6
 LOCUS AA463370 509 bp mRNA linear EST 10-JUN-1997
 DEFINITION zyx97412.r1 Soares,NhHMPU.S1 Homo sapiens cDNA clone IMAGE:811703 5'
 similar to SW:IL15_HUMAN P40933 INTERLEUKIN-15 PRECURSOR; mRNA
 sequence.
 ACCESSION AA463370
 VERSION AA463370.1 GI:2188254
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 509)
 AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Gelsel,G., Jost,S.,
 Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
 Schellenberg,K., Steptoe,M., Tan,F., Theisling,B., White,Y., Wyllie,
 T., Waterston,K. and Wilson,R.
 Washu-Merck EST Project 1997
 Unpublished (1997)
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 416.
 Location/Qualifiers
 1..509
 /organism="Homo sapiens"
 /db_xref="GDB:6042614"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:811703"
 /clone_lib="Soares_NhHMPU_S1"
 /tissue_type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /note="Organ: mixed (see below); Vector: pT73D-Pac
 (Pharmacia) with a modified polylinker; Site:1; Not I;
 Site:2; Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NBHM, pregnant uterus


```

/clone_lib="OT0030"
/dev_stage="Adult"
/note="Organ: ovary; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT      73 a      32 g      44 t
ORIGIN
Query Match      80.0%; Score 14.4; DB 9; Length 174;
Best Local Similarity 72.2%; Pred. No. 1.3e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY      1 AAYTGGGTAAATGATNATH 18
      111111111111111111
Db      145 AATTGGTTAATGTCATT 128

RESULT      2
BE315807/c
LOCUS
DEFINITION      BE315807 359 bp mRNA linear EST 21-DEC-2000
VERSION
ACCESSION      BE315807
KEYWORDS
SOURCE
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;
Medicago.
1 (bases 1 to 359)
Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula leaf library
Unpublished (2000)
On Jul 14, 2000 this sequence version replaced gi:9189584.
JOURNAL
COMMENT
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Medicago Genome Initiative accession: MGI:S:16165
Insert length: 688 Std Error: 0.00
Plate: 027 row: F column: 03
Seq primer: TCACACAGAAACAGCTATGAC.
FEATURES
source
1..359
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF027F031.F"
/clone_lib="Developing leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/note="Vector: lambda zap; Contains a mixture of very
young, developing, mature and senescing leaves."
BASE COUNT      91 a      102 c      52 g      114 t
ORIGIN
Query Match      80.0%; Score 14.4; DB 10; Length 359;
Best Local Similarity 72.2%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY      1 AAYTGGGTAAATGATNATH 18

```

```

Db      145  AATTGGGTGAACGTCATT 128

||||| ||||| ||||| |||
RESULT  3                                380 bp    mRNA       linear   EST 05-APR-1995
LOCUS   R08151/c
DEFINITION yf17h09.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone.
IMAGE=127169 3', mRNA sequence.
ACCESSION R08151
VERSION   R08151.1  GI:760074
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 380)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
          ,R., Williamson,A., Wohlmann,P. and Wilson,R.
The Mashu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert Size: 1556
High quality sequence stop: 249.
Location/Qualifiers
1..380
/oranism="Homo sapiens"
/db_xref="GDB:479330"
/db_xref="taxon:9606"
/clone="IMAGE:127169"
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pTF73D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
15' AACCTGCAGCAATTAATTAAGAAGCTTTTCTTTTTTTT 3',
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pTF73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Facilma Bonaldo."
BASE COUNT 111 a 73 c 86 g 109 t 1 others
ORIGIN

Query Match 80.0%; Score 14.4; DB 10; Length 380;
Best Local Similarity 72.2%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAATGGGTAAAYCYNATH 18
||:||||| ||:|| ||:
Db 227 AATTGGGTGAATGTCATC 210

RESULT  4                                487 bp    DNA        linear   GSS 16-OCT-1998
LOCUS   AO154673/c
DEFINITION HS_3021_A1_CO8_T7 CIT Approved Human Genomic Sperm Library D Homo
          sapiens genomic clone Plate=3021 Col=15 Row=E, DNA sequence.
```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 00:13:07 ; Search time 2591.91 Seconds
(without alignments)
93.732 Million cell updates/sec

Title: US-09-724-841-9
Perfect score: 18
Sequence: 1 AAYTGGTNAATGATNATH 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estov:*
6: em_estopl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.4	80.0	174	9	AM880392 QV0-OT003
C 2	14.4	80.0	359	10	BE315807
C 3	14.4	80.0	380	10	R08151
C 4	14.4	80.0	487	12	AO154673 HS_3021_A
C 5	14.4	80.0	490	12	AO132420 HS_3021_A
C 6	14.4	80.0	509	9	AA463370
C 7	14.4	80.0	515	10	BF650545
C 8	14.4	80.0	547	12	TA241H020
C 9	14.4	80.0	547	12	TA241H020
C 10	14.4	80.0	566	12	AM688129
C 11	14.4	80.0	584	10	BC0421826
C 12	14.4	80.0	600	12	BC082266 H3074C12-
C 13	14.4	80.0	609	12	AO947440 Sheared D
C 14	14.4	80.0	654	12	BH098364 RPCI-24-3
C 15	14.4	80.0	674	10	AO329420 nbx00044P
C 16	14.4	80.0	700	10	BF645513
C 17	14.4	80.0	709	12	BI271747 NF011A09F
					A2192227 SP_1020_B

18	14.4	80.0	765	12	AO859203	AO859203 nbep0011B
19	14.4	80.0	800	10	BC184658	BC184658 RST3720_A
20	14.4	80.0	838	10	BC069247	BC069247 H3074C12-
21	14.4	80.0	872	10	BI758686	BI758686 603024240
22	14.4	80.0	982	9	AL548180	AL548180 AL548180
23	14.4	80.0	994	9	AL572832	AL572832 AL572832
24	14.2	78.9	304	9	BA443796	BA443796 BA443796
25	14.2	78.9	393	12	AO990526	AO990526 Rfc01314
26	14.2	78.9	453	10	N40459	N40459 yv47e01.81
27	14.2	78.9	514	12	AQ408665	AQ408665 HS_5102_B
28	14.2	78.9	538	9	AI070145	AI070145 UT-R-Y0-1
29	14.2	78.9	566	12	AO991586	AO991586 Rfc02580
30	14.2	78.9	668	12	BS506964	BS506964 BS506964
31	14.2	78.9	689	12	AO990859	AO990859 Rfc01695
32	14.2	78.9	708	9	AV735264	AV735264 AV735264
33	14.2	78.9	735	12	AG029269	AG029269 Pan treg1
34	14.2	78.9	780	9	BE038814	BE038814 AB07C01_A
35	14.2	78.9	811	10	BC482190	BC482190 602526710
36	14.2	78.9	853	10	BE732877	BE732877 601567811
37	14.2	78.9	890	10	BF626046	BF626046 HV_CBA000
38	14.2	78.9	921	12	CNS03020	AL222909 Tetradon
39	13.4	74.4	123	9	AA559533	AA559533 MC070525
40	13.4	74.4	127	10	N25392	N25392 EST000062_S
41	13.4	74.4	140	9	AA931025	AA931025 SWTBADA00
42	13.4	74.4	140	10	H63019	H63019 EST000185_S
43	13.4	74.4	228	9	AM080888	AM080888 xc38b07_x
44	13.4	74.4	248	9	AA185820	AA185820 MAAD0147
45	13.4	74.4	249	9	AA140564	AA140564 MEEG0224

ALIGNMENTS

RESULT 1
LOCUS AM880392 174 bp mRNA linear EST 23-MAY-2000
DEFINITION QV0-OT0030-100400-188-a05 OT0030 Homo sapiens CDNA, mRNA sequence.
ACCESSION AM880392
VERSION AM880392.1 GI:8042402
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 174)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.G.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?fl=6t2-QV0-OT0030-100
400-188-a05&t3=2000-04-10&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 174.

FEATURES
source
1..174
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Wed Jun 19 09:14:04 2002

us-09-724-841-9.rng

Page 9

Job time: 5409 sec
